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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 23, 2001, 11:00:46 ; Search time 21.1 seconds
(without alignments)
3032.541 Million cell updates/sec

Title: US-09-587-574-1

Perfect score: 4445

Sequence: 1 MSSAVLVTLPPDPSSSFRED.....DETVLPMYEGRIIGKVERID 840

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4310	97.0	838	2 T08423	Axin homolog Ax11
2	1661	37.4	832	2 T08422	negative regulator
3	190.5	4.3	544	2 JC5503	G-protein signalin
4	189.5	4.3	519	2 S78089	G-protein signalin
5	173.5	3.9	1510	2 T33100	hypothetical prote
6	172.5	3.9	211	2 I53020	G-0/G-1 switch reg
7	167	3.8	173	2 S71812	RG510 protein - hu
8	163.5	3.7	533	2 T31002	hypothetical prote
9	161.5	3.6	181	2 JC7228	G-protein signalin
10	159	3.6	196	2 S43436	B cell activation
11	157.5	3.5	205	2 S78221	G-protein signalin
12	153.5	3.5	1023	2 T31669	neural zinc finger
13	151.5	3.4	1618	2 S21424	neural zinc finger
14	151	3.4	1150	2 S58775	myrl protein - smu
15	150	3.4	1032	2 T14124	neural zinc finger
16	149	3.4	2559	2 T09144	probable guanine n
17	148	3.3	1791	2 T02345	hypothetical prote
18	147	3.3	1200	2 A46194	neurofilament prot
19	143.5	3.2	1213	2 A58198	serine/proline-ric
20	143.5	3.2	1272	2 T30248	fragile X mental r
21	143.5	3.2	2416	2 T13825	adenomatous polypo
22	143	3.2	1383	2 T13052	guanine nucleotide
23	142.5	3.2	455	2 I48724	zinc finger protei
24	142.5	3.2	1210	2 I39410	AF-4 protein, spli
25	141	3.2	997	2 T28872	hypothetical prote
26	140	3.1	1677	2 T14267	hypothetical prote
27	139	3.1	284	2 T15700	hypothetical prote
28	138.5	3.1	1403	2 S24548	homeotic protein p
29	137	3.1	2688	2 I49477	alpha-A-crystallin

30	136.5	3.1	814	2 T26702	hypothetical prote
31	136.5	3.1	2464	1 Q8WSP1	microtubule-associ
32	136	3.1	1634	2 T26517	hypothetical prote
33	136	3.1	1655	2 T32633	hypothetical prote
34	135.5	3.0	1234	2 T30160	hypothetical prote
35	135.5	3.0	1507	2 B47328	natural killer cel
36	135.5	3.0	2298	2 T49648	hypothetical prote
37	134.5	3.0	1736	2 T00391	hypothetical prote
38	134.5	3.0	2722	2 T20532	hypothetical prote
39	134.5	3.0	3942	2 T42730	Basoon protein -
40	133.5	3.0	3924	2 S37431	ankyrin 2, neurona
41	132.5	3.0	1166	2 T13958	synGAP-b1 protein
42	132.5	3.0	1249	2 T14270	Ras-GTPase activat
43	132.5	3.0	1293	2 T14259	Ras-GTPase activat
44	132.5	3.0	1585	2 T31611	hypothetical prote
45	132.5	3.0	1983	2 T00385	KIAA0624 protein -

ALIGNMENTS

RESULT 1
T08423
Axin homolog Ax11 - rat
N:Alternate names: Ax11
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08423
R:Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, M.; Cell. Biol. 18, 2867-2875, 1998
A:Title: Ax11, a member of the Axin family, interacts with both glycogen synthase kin
A:Reference number: 216414; MUID:98226558
A:Accession: T08423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <YAM>
A:Cross-References: EMBL:AF017757; NID:93080758; PDB:AMC40089.1; PID:93080759
A:Note: interacts with GSK-3beta and beta-catenin
C:Keywords: phosphoprotein; signal transduction

Query Match	Score	DB 2:	Length	838:
Best Local Similarity	96.9%	Pred. No. 9.3e-265;		
Matches	814;	Conservative	7;	Mismatches 17; Indels 2; Gaps 1;
QY	1	MSSAVLVTLPPDPSSSFREDAPRPVPGEGETPPCQPSVGKQSTKPMVSSNARNED	60	
DB	1	MSSAVLVTLPPDPSSSFREDAPRPVPGEGETPPCQPSVGKQSTKPMVSSNARNED	60	
QY	61	GIQEPGRASPSPLTRMTKSLHSILGDODGAVLFTFLEREKCVDTLDFWFCNGFFROM	120	
DB	61	GIQEPGRASPSPLTRMTKSLHSILGDODGAVLFTFLEREKCVDTLDFWFCNGFFROM	120	
QY	121	NLKDTTLRVAAYRYEINNSVSKOLKPAKTYIRDGIRKQOIGSVMPDQACTEIOA	180	
DB	121	NLKDTTLRVAAYRYEINNSVSKOLKPAKTYIRDGIRKQOIGSVMPDQACTEIOA	180	
QY	181	VNEENAYQFLSDIYLEYVRSGENTAYMSNGCLSLVLCGYLPTLNEEBEWTCADLK	240	
DB	181	VNEENAYQFLSDIYLEYVRSGENTAYMSNGCLSLVLCGYLPTLNEEBEWTCADLK	240	
QY	241	CKTSPVVGSLSKTLRATASVSTEAENGFRSEFKSDVNPVHVGSGVFAPAISANDS	300	
DB	241	CKTSPVVGSLSKTLRATASVSTEAENGFRSEFKSDVNPVHVGSGVFAPAISANDS	300	
QY	301	ELSSDALTDSDSMTDSSVDGVPYRMGSKQLOREMHRSVKANGOVSLPHPRTRRLPK	360	
DB	301	ELSSDALTDSDSMTDSSVDGVPYRMGSKQLOREMHRSVKANGOVSLPHPRTRRLPK	360	
QY	361	EMTPVEPAAPAEILSRLEKLELESRLSLEERLOOIREDEKBESGQALSSRDGAPVO	420	
DB	361	EMTPVEPAAPAEILSRLEKLELESRLSLEERLOOIREDEKBESGQALSSRDGAPVO	420	

QY 600 -AAGPQL----PGEGRSDQVWQWMLEROSKSPHSAOSIRKSYPLESARAPGER 654
 DB 861 KAARSPVSHSHASEDEHREIOHSPASQNEAARSP-SVSHASHAHLEN-----HGGS 915
 QY 655 Y-----SHHLLGAGSH-----SRVARAHPTQ-----DP 680
 DB 916 LOSPVAASAGSHHMAESSEYTTSEKEISPSIFSSHTSEPOEQSONSPVASERDNRSF 975
 QY 681 AMPPLTPPTLAQLEBEACRRLAEVSK--POKQRC-CVASQ-----QDRNHSAGQAGAS 732
 DB 976 TRESSVTQMAAPLSPASDHAEOARESPSPFRAPSLHSQLSGNLEHNDENSAVVEAGOE 1035
 QY 733 PFANSLAPEDHKEPKKLASVHALDASE 760
 DB 1036 PATQSPIPLEQGRFRERASVNSQYASE 1063

RESULT 6
 153020
 G-0/G-1 switch regulatory protein 8 - human
 N:Alternate names: helix-loop-helix phosphoprotein; regulator of G-protein signaling 2,
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
 C:Accession: I53020; I65984
 R:Stiderovski, D.P.; Heximer, S.P.; Forsdyke, D.R.
 DNA Cell Biol. 13, 125-147, 1994
 A:Title: A human gene encoding a putative basic helix-loop-helix phosphoprotein whose m
 A:Reference number: I53020; MUID:94235158
 A:Accession: I53020
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-211 <RES>
 A:Cross-references: GB:LI3391; NID:g292036; PIDN:AAA20680.1; PID:g292037
 A:Accession: I65984
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-211 <RES>
 A:Cross-references: GB:LI3463; NID:g292054; PIDN:AAC37587.1; PID:g292055
 C:Genetics:
 A:Gene: GDB:RG52; G058
 A:Cross-references: GDB:355647; OMIM:600861
 A:Map position: Iq31
 A:Introns: 37/2; 71/2; 92/1; 147/3
 C:Superfamily: B-cell activation protein BL34
 C:Keywords: phosphoprotein

Query Match 3.9%; Score 172.5; DB 2; Length 211;
 Best Local Similarity 26.9%; Pred. No. 0.00066;
 Matches 46; Conservative 24; Mismatches 72; Indels 29; Gaps 4;
 QY 30 EGEPPPOPSVSGKYQV-----TKPMPVSSNARNRNDGCEPEGRASPDSPLTRWTKSLHSL 85
 DB 50 QNSSTPGPKPKGSKSQAQAFIKPSPEAQL-----WSEARDEL 87
 QY 86 LGDDGGALEFTFLEREKCVDTLDFWFCNGFROMNLKDTKLRAKAIKRYIENNSV 145
 DB 88 LASKYGLAFAFLKSEFCENIEFWLACEDFKTK-SPOLSKAKAKIYIDFEKEAPK 146
 QY 146 SKQLKPAKTYIRDGIRKQOIGSVMPDOAQTEIQAVMEENAYOVFLTSDIY 196
 DB 147 EINIDFQTKTLIAQNI--QEAISGCTTAAKRYVSLMENNISYPRFLESERY 195

RESULT 7
 S71812
 RGS10 protein - human
 C:Species: Homo sapiens (man)
 C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 17-Mar-1999
 C:Accession: S71812
 R:Shunt, T.W.; Fields, T.A.; Casey, P.J.; Peralta, E.G.
 Nature 383, 175-177, 1996

A:Title: RGS10 is a selective activator of Galpha(1) GTPase activity.
 A:Reference number: S71812; MUID:96371048
 A:Accession: S71812
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: mRNA
 A:Residues: 1-173 <HUN>
 C:Superfamily: B-cell activation protein BL34

Query Match 3.8%; Score 167; DB 2; Length 173;
 Best Local Similarity 31.8%; Pred. No. 0.0011;
 Matches 41; Conservative 32; Mismatches 52; Indels 4; Gaps 3;
 QY 77 RWTLSLHSLGDGAYLFTFLEREKCVDTLDFWFCNGFROMNLKDTKLRAKAIK 136
 DB 29 KWASLLENLEDPGAVKRFREFLKKESEENVLEWLACEDFKKQDK-TQMOEKAKITM 87
 QY 137 RYIENNSVSKQLKPAKTYIRDGIRKQOIGSVMPDOAQTEIQAVMEENAYOVFLTSDIY 196
 DB 88 TFL--SSKASSQVWEGQSRLNEKILEEP-HPLMFQKIQDQIFMLMKYDSYRFLKSDLF 144
 QY 197 LEYVRSGE 205
 DB 145 LKHRTIBE 153

RESULT 8
 T31002
 hypothetical protein F56B6.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T31002
 R:Stellies, L.; Stellye, L.
 submitted to the EMBL Data Library, September 1999
 A:Description: The sequence of C. elegans cosmid F56B6.
 A:Reference number: Z20957
 A:Accession: T31002
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-533 <STE>
 A:Cross-references: EMBL:U64599; PIDN:AAB04563.1
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Map position: X
 A:Introns: 39/3; 235/2; 259/2; 322/3; 360/2; 405/1; 461/3; 503/2
 A:Note: F56B6.2

Query Match 3.7%; Score 163.5; DB 2; Length 533;
 Best Local Similarity 30.3%; Pred. No. 0.009;
 Matches 40; Conservative 27; Mismatches 52; Indels 13; Gaps 4;
 QY 77 RWTLSLHSLGDGAYLFTFLEREKCVDTLDFWFCNGFROMNLKDTKLRAKAIK 134
 DB 392 QWEISFESLNNKFGCALPQFLKFESENMDFWLECEFEKM-KDGKSTQCAIET 449
 QY 135 YKRYIENNSV---VSKQLKPAKTYIRDGIRKQOIGSVMPDOAQTEIQAVMEENAYOV 190
 DB 450 YSEFVAHSEKSEVNLSDTRFAATKAIVAEAGKCPD-----TFALQSRVQLMSKDSYR 504
 QY 191 LTSDIYLEVRS 202
 DB 505 LRDRLFLDLES 516

RESULT 9
 JC7228
 G-protein signaling regulator 5 homolog - clawed frog
 C:Species: Xenopus sp. (clawed frog)
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
 C:Accession: JC7228; PC7066
 R:Saitoh, O.; Odagiri, M.; Masuno, I.; Nomoto, S.; Kinoshita, N.
 Biochem. Biophys. Res. Commun. 270, 34-39, 2000


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Query Match      3.58; Score 153.5; DB 2; Length 1023;
Best Local Similarity 20.7%; Pred. No. 0.097;
Matches 152; Conservative 82; Mismatches 230; Indels 271; Gaps 38;

QY 198 EYVSGGENTPAAVMNGSGISLVLGGLPTLNEEEMTCADLKCKSLPTVGLSSKTLRA 257
      | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 119 ESVQTVGEN--LNGNGIQSLKAC-----DEANE-----CFM-----148

QY 258 TASVRSLETENGRFSKRSDPVNPVHGSGYFAPATSAENSELSDALTDMSMTDS 317
      | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 149 -----EHSDDGDKVHNSQP-----PCCSGDSESDSDNTENGSGCSNS 188

QY 318 SYDGVPEYRMGSKKROL--OREMHR--SYKANGOVSLPHRPRIHRLKEMTPVPEPAFAA 372
      | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 189 SED--PTTHNGPRKRLTYNKKDLLEVPETKAEDD--KTIPEKRCSDSDTSGADPNSHM 243

QY 373 ELIS-RLEKLKLELSNHSLEERLOQIREDEKGS-----EQ--ALSSRDGAPVQHPIAL 425
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 244 EPLSVKQSPFPEVEESESATVIAESAEVEKAKGSLLEQALALQAEAGSVFHH-----299

QY 426 LPSGSEVEDQTLDDHLSRVLKTPEGQSQVGR-----YSRSPSPDHHNNHHHQQC 479
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 300 -----TKELDRFL-DELAQRORQKV-IDASGRQIIFNNKHSR-----PERE-----342

QY 480 HTLLSTGKLPVPAACRYLGGKSEFLTKQTKNHNHNYIHNAVR-----KKEEIEAETQ 535
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 343 -----AKCPIPGCDG-----TGHTGLYLRHNRSLSGCPKHYRVLELLAHN 383

QY 536 RVKSLCGRGTDYYCYSKCKSHPKARELPGEQFCGSRGTLPRKNAKGTETGLALSARDG 595
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 384 ENVLKC-----PTPG--CTGRGHVNSNRNTHRSLSGCPIAAEK 420

QY 596 -----GMSSAAGRPOLPGEEDRSODVWQ-----WMLSEERQSKSPH-----633
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 421 LAMTQDKSOLDSSQTOGR---EQAHRYVLVQKQIEFNRSQAITPRKASASEQKFGK 476

QY 634 -----SAOSTRKSTPLESARA--APGBVSRHH-----LLGASGHSRYAARAH 674
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 477 VPEDVASFQAQVFKRPLLOTGGOKAPPEPESKHFNSPVKFSNGILPSAGAHQSTVTRAS 536

QY 675 -----PFTODPAPRLTPNTLAOLEACRRLAEV--SKPOKORCVASQODRN-----722
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 537 SYVGHQGYSD--THIAAAAAILNLSTRCREATDILSNKPSQILAKGAEIEVDENGTDL 593

QY 723 -----HSAAGQAGASPFPANPSIAP-----741
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 594 SMKNNRILDKSIGCTSSHTTITATPSSSPFKASLLVNAFYQALCDQEGMNPINYSKSH 653

QY 742 ---EDHKKEPKKLASVALQASELVITYFFCGE-EIP-----YRMLKAKQSITL-----785
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 654 GKTEEKKEDPVNSENLEKK-----FAGEASIPSPKPKLHTLDLKKELITCPTPGCD 707

QY 786 --GHFEQQLSKKGNV 798
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 708 GSGHV-----TGNY 716

RESULT 13
S21424
nestin - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C:Accession: S21424
R:DaHlstrand, J.; McKay, R.D.G.; Zimmerman, L.B.; Lendahl, U.
submitted to the EMBL Data Library, May 1992
A:Description: Characterization of the human nestin gene reveals a close evolutionary re
A:Reference number: S21424
A:Accession: S21424
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1618 <DAH>

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Tue Oct 23 15:36:23 2001

us-09-587-574-1.rpt

Page 8

Search completed: October 23, 2001, 11:03:18
Job time: 152 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 23, 2001, 11:00:11 ; Search time 13.99 Seconds
(without alignments)
1236.304 Million cell updates/sec

Title: US-09-587-574-1

Perfect score: 4445
Sequence: 1 MSSAVLVTLPPDSSSFRED.....DETVLPMYEGRIIGKVERID 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
- No.							
1	172.5	3.9	211	2	US-08-748-483-4		Sequence 4, Appl1
2	170.5	3.8	243	2	US-08-829-110-3		Sequence 3, Appl1
3	166	3.7	119	2	US-08-588-258B-31		Sequence 31, Appl1
4	166	3.7	119	3	US-08-460-505-31		Sequence 31, Appl1
5	166	3.7	119	5	PCT-US96-08295-31		Sequence 31, Appl1
6	166	3.7	196	2	US-08-829-110-5		Sequence 5, Appl1
7	166	3.7	196	2	US-08-748-483-3		Sequence 3, Appl1
8	162.5	3.7	1182	4	US-09-041-886-21		Sequence 21, Appl1
9	159	3.6	181	2	US-08-748-483-1		Sequence 1, Appl1
10	158	3.6	121	2	US-08-588-258B-32		Sequence 32, Appl1
11	158	3.6	121	3	US-08-460-505-32		Sequence 32, Appl1
12	158	3.6	121	5	PCT-US96-08295-32		Sequence 32, Appl1
13	157.5	3.5	205	2	US-08-829-110-6		Sequence 6, Appl1
14	157.5	3.5	205	2	US-08-748-483-5		Sequence 5, Appl1
15	152	3.4	159	2	US-08-829-110-1		Sequence 1, Appl1
16	151.5	3.4	1618	1	US-07-853-913-4		Sequence 4, Appl1
17	149	3.4	2509	2	US-08-149-097D-35		Sequence 35, Appl1
18	146.5	3.3	202	1	US-08-724-318-2		Sequence 2, Appl1
19	146.5	3.3	202	2	US-08-463-081B-2		Sequence 2, Appl1
20	146.5	3.3	202	2	US-08-461-379A-2		Sequence 2, Appl1
21	146.5	3.3	202	2	US-08-462-390B-2		Sequence 2, Appl1
22	146.5	3.3	202	2	US-08-754-108-2		Sequence 2, Appl1
23	146.5	3.3	202	3	US-08-870-815-4		Sequence 4, Appl1
24	146.5	3.3	202	3	US-08-463-074B-2		Sequence 2, Appl1
25	146.5	3.3	202	3	US-08-465-585C-2		Sequence 2, Appl1
26	146.5	3.3	202	3	US-08-652-446-2		Sequence 2, Appl1
27	146.5	3.3	202	4	US-08-949-004-4		Sequence 4, Appl1

28	146.5	3.3	570	3	US-08-826-246-2	Sequence 2, Appl1
29	146.5	3.3	570	3	US-08-944-495-2	Sequence 2, Appl1
30	146.5	3.3	570	3	US-09-126-640-7	Sequence 7, Appl1
31	146.5	3.3	570	4	US-08-925-588-2	Sequence 2, Appl1
32	143.5	3.2	201	2	US-08-726-228-2	Sequence 2, Appl1
33	143.5	3.2	201	3	US-08-870-815-2	Sequence 2, Appl1
34	143.5	3.2	201	4	US-08-949-004-2	Sequence 2, Appl1
35	142.5	3.2	1187	1	US-08-320-559-28	Sequence 28, Appl1
36	142.5	3.2	1187	3	US-08-545-860D-28	Sequence 28, Appl1
37	142.5	3.2	1187	5	PCT-US94-04496-28	Sequence 26, Appl1
38	142.5	3.2	1210	1	US-08-320-559-26	Sequence 26, Appl1
39	142.5	3.2	1210	5	US-08-545-860D-26	Sequence 26, Appl1
40	142.5	3.2	1210	5	PCT-US94-04496-26	Sequence 26, Appl1
41	135	3.0	123	2	US-08-588-258B-39	Sequence 39, Appl1
42	135	3.0	123	5	PCT-US96-08295-39	Sequence 39, Appl1
43	131.5	3.0	2441	1	US-08-194-468-2	Sequence 2, Appl1
44	131.5	3.0	2441	3	US-08-961-739-2	Sequence 2, Appl1
45	128.5	2.9	763	4	US-08-961-083-66	Sequence 66, Appl1

ALIGNMENTS

RESULT 1
US-08-748-483-4
Sequence 4, Application US/08748483
Patent No. 5955314
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,483
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0157 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 292037
US-08-748-483-4
Query Match 3.9%; Score 172.5; DB 2; Length 211;
Best Local Similarity 26.9%; Pred. No. 1.3e-07;

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01 RESULT      2
02 US-08-829-110-3
03 Sequence 3, Application US/08829110
04 Patent No. 5882890
05 GENERAL INFORMATION:
06 APPLICANT: Hillman, Jennifer L.
07 TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
08 NUMBER OF SEQUENCES: 6
09 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Incyte Pharmaceuticals, Inc.
11 STREET: 3174 Porter Drive
12 CITY: Palo Alto
13 STATE: CA
14 COUNTRY: USA
15 ZIP: 94304
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Diskette
18 COMPUTER: IBM Compatible
19 OPERATING SYSTEM: DOS
20 SOFTWARE: FASTSEQ for Windows Version 2.0
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/829,110
23 FILING DATE: Filed Herewith
24 CLASSIFICATION: 514
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:
27 FILING DATE:
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Billings, Lucy J.
30 REGISTRATION NUMBER: 36,749
31 REFERENCE/DOCKET NUMBER: PF-0259 US
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 415-855-0555
34 TELEFAX: 415-845-4166
35 INFORMATION FOR SEQ ID NO: 3:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 243 amino acids
38 TYPE: amino acid
39 STRANDEDNESS: single
40 TOPOLOGY: linear
41 IMMEDIATE SOURCE:
42 LIBRARY: THYMNOTO2
43 CLONE: 343504
44 US-08-829-110-3
45
46 Query Match          3.88; Score 170.5; DB 2; Length 243;
47 Best Local Similarity 28.1%; Pred. No. 2.4e-07;
48 Matches 55; Conservative 38; Mismatches 78; Indels 25; Gaps
49
50 14 SSSFFEDAPRPVVGEEBETPPQCPGVGXQSTKPKPVSSNARRNDGLGPEEGRASD- 72
51   | ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
52 49 SHFFELAE-----EEAQGLRASP-----EDAKP-----AMRPPSDIHSDSSSSSH 91
53   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
54 73 --SPLTWTKSLHSLGDODGAVLFTFLERREKCVDTIDFWACNGFRONMLTDYTLR 129

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RESULT      3
US-08-588-258B-31
; Sequence 31, Application US/08588258B
; Patent No. 5929207
; GENERAL INFORMATION:
; APPLICANT: H. Robert Horvitz et al.
; TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,258B
; FILING DATE: January 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 01997/216001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-588-258B-31

Query Match      3.7%; Score 166; DB 2; Length 119;
Best Local Similarity 32.5%; Pred. No. 1.9e-07;
Matches 40; Conservative 29; Mismatches 46; Indels 8; Gaps 3;

DB      QY      77      RMTKSLSHSLGQDDAYLFFETLEBEKCVDTLDWPAFCNGPR--QWMLKDTKTLRYAKAI 134
      QY      1   QMSQSLTEKLINQIQNVQVGFSLKSEFSEENIEFWLACEDIKKTESDLPCK---AEET 56
      DB      QY      135  YKRYTEIENNSVSKQLPKPATKYIIRDKIKQOIGSMFQDAQTEIOLVMEENAYQVFLTSD 194
      DB      QY      57  YKAFVHSDA--AKQINIDFPRRESTAKIKAPPTTCGDEAQYIYTLMEQDSIPRLKSD 114
      QY      195  IYL 197
      DB      QY      115  IYL 117

RESULT      4
US-08-460-505-31
Sequence 31, Application US/08460505

```

```

; Patent No. 6069296
; GENERAL INFORMATION:
; APPLICANT: Horvitz, Robert H.
; APPLICANT: Koelle, Michael
; TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALING
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,505
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 01997/214001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-505-31

Query Match 3.7%; Score 166; DB 3; Length 119;
Best Local Similarity 32.5%; Pred. No. 1.9e-07;
Matches 40; Conservative 29; Mismatches 46; Indels 8; Gaps 3;

QY 77 RWTGSHSLGDDGAYLRTFLERKCVDTLDFWACNGFR--QNLKDTFLRAKAI 134
DB 1 QWSQSLKRLAQTQNVGSGFLKSESENEFWLACEDYKTESDLLPCR---AEEI 56
QY 135 YKRYIENNSVSKQLPATKYIRDGIRKQKQIGSVFDPQAGTEIQVMEENAYQVELTSD 194
DB 57 YKAFVHSDA-AKQINIDRTRESTAKKIKAPPTPCFDEAKQVYITLMKDSYPRLKSD 114
QY 195 IYL 197
DB 115 IYL 117

RESULT 5
PCT-US96-08295-31
; Sequence 31, Application PC/TUS9608295
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALING
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08295
; FILING DATE: 31-MAY-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/588,258
; FILING DATE: 12-JAN-96
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 01997/216001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-08295-31

Query Match 3.7%; Score 166; DB 5; Length 119;
Best Local Similarity 32.5%; Pred. No. 1.9e-07;
Matches 40; Conservative 29; Mismatches 46; Indels 8; Gaps 3;

QY 77 RWTGSHSLGDDGAYLRTFLERKCVDTLDFWACNGFR--QNLKDTFLRAKAI 134
DB 1 QWSQSLKRLAQTQNVGSGFLKSESENEFWLACEDYKTESDLLPCR---AEEI 56
QY 135 YKRYIENNSVSKQLPATKYIRDGIRKQKQIGSVFDPQAGTEIQVMEENAYQVELTSD 194
DB 57 YKAFVHSDA-AKQINIDRTRESTAKKIKAPPTPCFDEAKQVYITLMKDSYPRLKSD 114
QY 195 IYL 197
DB 115 IYL 117

RESULT 6
US-08-829-110-5
; Sequence 5, Application US/08829110
; Patent No. 5882890
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goll, Surya K.
; TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
; SIGNALING
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,110
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

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Query Match 3.7%; Score 162.5; DB 4; Length 1182;

Best Local Similarity 21.18; Pred. No. 1.8e-05;
Matches 102; Conservative 49; Mismatches 177; Indels 155; Gaps 21.

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OY 274 FKRDVPRNVUGS-GUVFAPATS-----ANDSEL--SDALNDDDSMW-----TDS 312
Dd 676 FORNERPSPTJEGGRCGNALPSTOLDRCGLMANSGLKSPWVJORAQEMFOKTGTS 735
OY 318 SVDDVPRYMGSKKLOD-----REMHRS-----VKANQO---VLPNPRPTNRLPKPM 362
Dd 736 PEGRRPRDMPRMSQNSGVEMREKRGDSYSDSEHULYMEGOGRAAMRLPRAENOTISOT 795
OY 363 TPVEPRAFAAELISR-----LEKLELESRSLSLEBRLOQITREDEKBSGQALSSRDG 416
Dd 796 SPMKRSASVLPGRKARRLDYSLERVPREENQRH-----HQRDRDSHRSASERSL----- 844
OY 417 APVGNPLALLPSGSEEDPQTITLDDHLSRVLTKTRPGSOPVSGVSPRSRSDNNHONNNH 476
Dd 845 -----GRY-TRDVTGTCTDLS--MTTQSGDLBSKEDQERGRKDKKKNHNN 889
OY 477 QOCHTLTLSTGGLRPRVACSLGSGKSFLLKQTKKNHNNYNNHNAVTKTELEATOR 536
Dd 890 -----NNNN-NHNNRRPRRQDAQGRPH 912
OY 537 VRCLSPGSTDYUCYSKKCSHKPKARELPYRGDFGSGRSGTLPKNAKGTERRGLALSARDG 596
Dd 913 GR-----ARARDRWSRSPSEGREHNAHRGSS-----SSVSGSPAPSTSGT 953
OY 597 MSSAAGPOLP-----GEGDNRDVMQWMLSEHQSKKP-HSQD 636
Dd 954 STRPRGRROLRQTPSTRPRNVYSVPYIRKAGSGRPQQ--QOQOQOQOQOQAVAPERRAT 101
OY 637 SIRKSYPLESARAAPGSEVRGNHNLGASGHSRSVAVARANPTODRAPMLPTPLTGLQEE 696
Dd 1012 SGPRRYGCPRAEPAGRRP-----TGGHSSG-----RSPRMERVRPGTARBSFR 105
OY 697 ACR 699
Dd 1058 ACR 1060

RESULT 9
US-08-748-483-1
: Sequence 1, Application US/08748483
: Patent No. 5955314
: - GENERAL INFORMATION:
: APPLICANT: HILMAN, Jennifer L.
: APPLICANT: GOLL, Surya K.
: TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: US
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/748,483
: FILING DATE: Herewith
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0157 US
: TELECOMMUNICATION INFORMATION:
:

```

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: TELEPHONE: 415-855-0555
: TELFAX: 415-845-4166
:
: TELEX:
:
: INFORMATION FOR SEQ ID NO:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 181 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: Consensus
: CLONE: 57362
:
: JS-08-748-483-1

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Query Match	3.6%	Score 159;	DB 2;	Length 181;
Best Local Similarity	29.1%;	Pred. No. 1.6e-06;		
Matches 39;	Conservative 28;	Mismatches 63;	Indels 4;	Gaps 3;

Qy	68	RASDPSLPTRTKTSJHSLSGQDQAYLPRTFLEREKCVDTLIDFWFACNGRÖMLKOTKT	127
Db	52	KTSLDEAL-QWRDSDLKDLKLNQNYSLASFSEKSEFSEENEFWIAEDYKKIK-SPAK	109
Oy	128	LRAKAIYKRIENNSVSKOLKPATKTYINDGJKKQIGSWFDOAQTEIOAWMEENAY	187
Db	110	AEKAQOIYEETIÖTAPAEVNIDHPTKDTYKNIIVPSLSL--PDMQKRIHALMERDST	167
Oy	188	QVFLTSDIYLEYVR	201
Db	168	PRFVRSFEYQELIK	181

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10 RESULT
11 US-08-588-258B-32
12 ; Sequence 32, Application US/08588258B
13 ; Patent No. 5929207
14 ; GENERAL INFORMATION:
15 ; APPLICANT: H. Robert Horvitz et al.
16 ; TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
17 ; NUMBER OF SEQUENCES: 41
18 ; CORRESPONDENCE ADDRESS:
19 ; ADDRESSEE: Clark & Elbing LLP
20 ; STREET: 176 Federal Street
21 ; CITY: Boston
22 ; STATE: MA
23 ; COUNTRY: USA
24 ; ZIP: 02110
25 ; COMPUTER READABLE FORM:
26 ; MEDIUM TYPE: Floppy disk
27 ; COMPUTER: IBM PC compatible
28 ; OPERATING SYSTEM: Windows 95
29 ; SOFTWARE: FastSeq Version 2.0
30 ; CURRENT APPLICATION DATA:
31 ; APPLICATION NUMBER: US/08/588,258B
32 ; FILING DATE: January 12, 1996
33 ; CLASSIFICATION: 435
34 ; ATTORNEY/AGENT INFORMATION:
35 ; NAME: Bieker-Brady, Kristina
36 ; REGISTRATION NUMBER: 39,109
37 ; REFERENCE/DOCKET NUMBER: 01997/216001
38 ; TELECOMMUNICATION INFORMATION:
39 ; TELEPHONE: 617-428-7045
40 ; TELEFAX: 617-428-7045
41 ; TELEX:
42 ; INFORMATION FOR SEQ. ID NO.: 32:
43 ; SEQUENCE CHARACTERISTICS:
44 ; LENGTH: 121 amino acids
45 ; TYPE: amino acid
46 ; STRANDEDNESS: not relevant
47 ; TOPOLOGY: linear
48 ; MOLECULE TYPE: protein
49 ;
50 US-08-588-258B-32

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 23, 2001, 10:57:16 ; Search time 25.04 Seconds
(without alignments)
2033.712 Million cell updates/sec

Title: US-09-587-574-1
Perfect score: 4445
Sequence: 1 MSSAVLVTLPPSSSFRED.....DETLPWEGRIIGKVERID 840

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
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22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4445	100.0	840	AAW93570	Human conductin pr
2	4445	100.0	840	AAW93569	Human conductin pr
3	1655	37.2	992	AAW96265	Murine axin. Mus
4	1605	36.1	900	AAW96264	Human axin. Homo
5	208	4.7	235	AAW97153	Human regulator of
6	193	4.3	235	AAW97154	Murine regulator o
7	172.5	3.9	220	AAW56929	Human prostate can
8	170.5	3.8	243	AAW30561	Human regulator of
9	168	3.8	181	AAW44834	Human p26 protein.
10	168	3.8	207	AAW54360	Human pancreatic c
11	167.5	3.8	116	AAW41020	RGS2 protein RGS r

12	166	3.7	196	22	AAW76863	Human lung tumour
13	166	3.7	217	20	AAW43847	Human cancer assoc
14	164.5	3.7	116	20	AAW41021	RGS3 protein RGS r
15	164	3.7	181	19	AAW44833	Rat p26 protein se
16	162.5	3.7	1182	20	AAW33496	Human SCA6 protein
17	161	3.6	115	20	AAW41019	RGS1 protein RGS r
18	161	3.6	181	19	AAW44835	Mouse p26 protein.
19	159	3.6	181	19	AAW62075	Human regulator of
20	159	3.6	181	21	AAW53931	A human regulator
21	156.5	3.5	118	20	AAW41001	Mouse RGS2 protein
22	155.5	3.5	1618	13	AAW27205	Human nestin. Hom
23	153	3.4	115	20	AAW41024	RGS10 protein RGS
24	152.5	3.4	118	20	AAW41000	Rat RGS4 protein R
25	152	3.4	159	19	AAW30560	Human regulator of
26	151.5	3.4	1618	15	AAW60127	Human nestin prote
27	151	3.4	2559	20	AAW41012	Amino acid sequenc
28	149	3.4	2510	16	AAW71007	Human neuronal cal
29	149	3.4	2510	16	AAW10579	Human calcium chan
30	146.5	3.3	116	20	AAW41022	RGS4 protein RGS r
31	146.5	3.3	202	17	AAW89895	p53 response prote
32	146.5	3.3	202	18	AAW08133	Human cytokine res
33	146.5	3.3	202	19	AAW59294	Human RATH1.1 prot
34	146.5	3.3	202	21	AAW87952	Human CR1 protein.
35	146.5	3.3	570	18	AAW36002	Human Fchd531 gene
36	146.5	3.3	570	21	AAW45013	Protein encoded by
37	146	3.3	3266	21	AAW42491	Human ORFX ORF2255
38	144.5	3.3	2608	21	AAW85574	HS-UNC-53.3/GFP f
39	143.5	3.2	201	19	AAW58293	Mouse RATH1.1 prot
40	143	3.2	2385	21	AAW85569	Human homologue of
41	142.5	3.2	1187	16	AAW66451	AF-4 protein (enco
42	142.5	3.2	1210	16	AAW66450	AF-4 protein (enco
43	139.5	3.1	116	20	AAW41028	Human GAI protein
44	139.5	3.1	2091	21	AAW12000	Rat p3103 protein.
45	139	3.1	2432	21	AAW85565	Human homologue of

ALIGNMENTS

RESULT 1	
ID	AAW93570 standard; Protein; 840 AA.
AAW93570:	
AC	AAW93570:
XX	
DT	17-JUN-1999 (first entry)
XX	
DE	Human conductin protein.
XX	
KM	Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW	therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KM	Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
KW	tumour suppressor.
XX	
OS	Homo sapiens.
XX	
PM	W09911780-A2.
XX	
PD	11-MAR-1999.
XX	
PF	01-SEP-1998; 98MO-DE02621.
XX	
PR	02-SEP-1997; 97DE-1038205.
XX	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX	
PI	Behrens J, Birchmeier W;
XX	
DR	WPI. 1999-214706/18.
XX	
DR	N-PSDB; AAX23370.
XX	
PT	Tumour-suppressing protein conductin - used for treatment and
	diagnosis of tumors

xx Claim 11; Fig 3; 22pp; German.

cc This invention describes a novel human conductin protein which has
cc anti-tumour activity. Detecting the presence or amount of conductin,
cc at protein or nucleic acid levels, is used to diagnose tumours, while
cc agents that (re)activate conductin are used for tumour therapy.
cc Conductin binds to beta-catenin and induces its cytoplasmic degradation,
cc resulting in blockade of the Wnt/Wingless signalling pathway in
cc vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
cc fragments and, in conjunction with APC, acts as a tumour suppressor.

xx Sequence 840 AA;

Query Match 100.0%; Score 4445; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSAVLVTLPPSSSFRDAPRPVPEEGETPPCOPSVGVOSTKMPVSSNARNED 60
DB 1 mssavlvtlppsssfredaprpvpgegetppcqpqsvgvtkmpvssarnred 60
QY 61 GIGEEGASPPSPRTWTKSLHSLGQDQAYLFRTRLEKRCVDTLDEFACNGFRQ 120
DB 61 gigeegaspsprtwtkslhslgqdqaylfrtrlekrctvdtldefacngfrqm 120
QY 121 NLKDKTRVAKAIKRYIENNSVSKOLKPKATKTYIRDGIRKQOIGSVMPDOAQTEIO 180
DB 121 nlkdktrvakaiarkyiennsvskolkpkatkyirdgirkqoigsvmpdoaqteio 180
QY 181 VMEENAYVFLTSDIYLYVSGGENTAYMSGIGSLKVLGYLPTLNEEWTCADLK 240
DB 181 vmeenayvfltsdiylvysggentaymsgigslkvlgylptlneewtcadlk 240
QY 241 CKLSPTVVGSLSKTRATASVSTETANGFRSPDPVPHVSGVYAPATSAANDS 300
DB 241 cklsptvvgslsktratastvstetangfrspdpvphvsgvyapatsaands 300
QY 301 ELSSDALTDSSMSMTDSSVDGVPYRMGSKOLOREHRSVYKANGOVSLPHFPTHRLPK 360
DB 301 elssdaltdssmsmtdssvdgvpymrgskolorehrrsvykanogvslphfpthrlpk 360
QY 361 EMTVEPAFAELISRLKLEKLESHSLERLQOUREBEKSGSQAISRDGAPVQ 420
DB 361 emtvepafaellisrlklekleshslerlqourebeeksgsqaalsrdgapvq 420
QY 421 HPALALPSGSYEEDPOTLLDHLRLVLTQPCQSPGVGRYSPRSRSPDHQHOOCH 480
DB 421 hpalalpsgsyeedpotlldhlrlvltqpcqspgygrysprsrspdhqhooch 480
QY 481 TLLESTGKLPVAAACPLLGKSFLLTKOTTKVHHHYIHHNAVPTKEIEEATQRYVCL 540
DB 481 tllstgklpvaaacpllgksflltkottkvhhhyihhnavptkeieeatqrvcl 540
QY 541 CPGSTDYVCYKSKSHKAPRPLPGEOFCGSGTLPRKNAKGEPLGIALSARGGSSA 600
DB 541 cpgstdyvcyskshkapeplpggefcsgrgtlprknakgeplgialsaraggssa 600
QY 601 AGGFOLPGEEDRSQDWOMWLESEKSKSPHSAQSIIRKSYPLESARAAGEVSRHHL 660
DB 601 aggfplgeegdrsqdwomwleseksksphsaqsiirksyplesaraagevsrhhl 660
QY 661 LGASGHSRVARAHPTQDPAMPPLPNTLAQLEACRLAEVSKPOKORCCVASOORD 720
DB 661 lgasghsrvarahptqdpampplpntlaqleacrrlaevskpokrccvasoord 720
QY 721 RNSAAGACGASPPANSILAPEDHKPKKLASVALASSELVYTFYFCGGEIPIRRMLKA 780
DB 721 rnsaagacgasppansilapedhkpkklasvalasaselvytfyfcggeipirrmlka 780
QY 781 QSLTLGHFKKQSKGNRYRYFKASDEFACGAFEEIMDETVLPMYEEIRILGKVERID 840
DB 781 qsltlghfkkskgnryryfkasdefacgafeeimdetvlpmyeeriigkverid 840

DB 781 qsltlghfkkskgnryryfkasdefacgafeeimdetvlpmyeeriigkverid 840

RESULT 2

AAW93569
ID AAW93569 standard; Protein: 840 AA.

AAW93569;

17-JUN-1999 (first entry)

Human conductin protein.

KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
KW Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
KW tumour suppressor.

OS Homo sapiens.

FT Key Location/Qualifiers
FT Domain 78..200

FT /note= "Regulator of G protein signalling domain as
FT Binding-site 343..396 described in claim 12"

FT /note= "GSK 3-beta binding region as described in
FT Binding-site 397..465 claim 13"

FT /note= "Beta-catenin binding domain as described in
FT Region 783..833 claim 14"

FT /note= "Dishevelled homology region as described in
FT claim 15"

PN NO9911780-A2.

PD 11-MAR-1999.

PF 01-SEP-1998; 98WO-DE02621.

PR 02-SEP-1997; 97DE-1038205.

PA (DELB-) DELBROECK CENT MOLEKULARE MEDIZIN MAX.

PI Behrens J, Birchmeier W;

DR WPI: 1999-214706/18.

DR N-PDB; AAX23369.

PT Tumor-suppressing protein conductin - used for treatment and
PT diagnosis of tumors

PS Claim 11; Fig 1; 22pp; German.

cc This invention describes a novel human conductin protein which has
cc anti-tumour activity. Detecting the presence or amount of conductin,
cc at protein or nucleic acid levels, is used to diagnose tumours, while
cc agents that (re)activate conductin are used for tumour therapy.
cc Conductin binds to beta-catenin and induces its cytoplasmic degradation,
cc resulting in blockade of the Wnt/Wingless signalling pathway in
cc vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
cc fragments and, in conjunction with APC, acts as a tumour suppressor.

xx Sequence 840 AA;

Query Match 100.0%; Score 4445; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSAVLVTLPPSSSFRDAPRPVPEEGETPPCOPSVGVOSTKMPVSSNARNED 60
DB 1 mssavlvtlppsssfredaprpvpgegetppcqpqsvgvtkmpvssarnred 60

OY 61 GIGPEGRASPSPLTRMTKSLHSLGDDGAYLFRFLEREKCVDTLDFWACNGFROM 120
DB 61 g1gepegaspspltrmtkshslgddgaylfrflerekcvdtldfwacngftrqm 120
OY 121 NLKDKRTLRVAKAIYKRYIENNSVSKOLKPKATKYIRIDGIKKOOIGSMFDOAOTEIOA 180
DB 121 nlkdkrtlrvakaiykyriennsvskolkpkatkylridgikkgiigsmfdaqteiq 180
OY 181 VMEENAVOFLTSIDYLEYVNSGGENTAYMNSGGLSKVLGCGYPTLNNEEEMTCADIK 240
DB 181 vmeenavofltsidyleyvrnsgeentaemngslgskvlcgypnlneeevctadik 240
OY 241 CKLSPTVVGSLSKTLRATASVSRSTETAEANGFRSRSDPVNVAHNGSCYVFAPATSANDS 300
DB 241 cklsptvvgslsktlratasvrsstetaeangfrsrdpvnvahnngscyvfapatsands 300
OY 301 ELSSDALTDMSMTSSVDGVPRYRMGSKKOLQREHMRSVKANGQVSLPHFPRTRRLPK 360
DB 301 elssdaltdmsmtssvdgvprymgskkqlqremhmrsvkangqvslphfprtrrlpk 360
OY 361 EMTPEPAFAAEELISRLKLEKLESHNSLEERLQOIREDEKESQALSSRDGARVQ 420
DB 361 emtpepaafaellisrllekleshnsleerlqlredeekesqalsrdgarvq 420
OY 421 HPLALLPBGSGYEEDPQTLDDHLSLVLTFRGCGSPGVGRYSRSPSRPNHNNHNNQCH 480
DB 421 hplallpbgsgyeedpqtllddhlsvlvtfrgcspgvgrysrpsrpnhnnhnnqch 480
OY 481 TLLSTGGLRPAACPLRLGSGSFLTKQTTKHNHNHYNHNHNAVPKKEETAEATORVRL 540
DB 481 tllstggllrpaacplrlgsgsfltkqttkhnhnynhnhnnavpkkeetaeatorvrl 540
OY 541 CPGGTDYTCYSKCKSHKPAERLPEDQFCGSRGTLPKRNAGTEPGLALSADGMSA 600
DB 541 cpggtdytcyskckshkpaerlpedqfcgsrgtllpkrnagtepglalsadgmsa 600
OY 601 AGCPOLPEEEDRQDVMQWMLSESRQSKSPHSNOSTIRKSVPLSARAPEREYSRHL 660
DB 601 agcpolpeeedrqdvmqwmlesesrqsksphsnostirksvplsarapereysrhl 660
OY 661 LGASGHSVAVRANHPOTDPAHPPLTPNTLAQLEACRRLAEVSKPKORCCVASQORD 720
DB 661 lgasghsvavaranhpotdpaamppltpntlaqlaeacrrlaevskpkorcvasqord 720
OY 721 RNHSAGAGASPRANPSLAPEDHKEPKKLASVALQASELVVTFPCGEEIPYRMLKA 780
DB 721 rnhsagagasprianpslapedhkepkklasvalqaselvvtfpcgeeiptyrmlka 780
OY 781 OSLTGHKREOLSKGNRYVFKKASDEPACGAVFEETIMDDETVLPMBGRILGVERID 840
DB 781 osltghkreqlskgnryyfkksdelacgavfeetlmdetvlpmyegrilgverid 840

RESULT 3
AAM96265
ID AAM96265 standard: Protein: 992 AA.

XX AAM96265;
XX 14-JUN-1999 (first entry)
XX DT
XX DE Murtine axin.
XX AXIN: cancer; breast cancer; colorectal cancer;
KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
KW beta-catenin.
XX OS Mus musculus.
XX PN M09902179-A1.
XX

PD 21-JAN-1999.
XX
XX 09-JUL-1998; 98WO-US14414.
XX PF
XX 10-JUL-1997; 97US-0890865.
XX PR
XX PA (UYCO) UNIV COLUMBIA NEW YORK.
XX PI Constantini F, Zeng L;
XX WP1: 1999-120510/10.
XX DR N-PSDB; AAX09013.
XX
PT Newly isolated nucleic acid encoding "axis inhibition" protein
PI (Axin) - useful for detecting, diagnosing and treating cancer
XX
PS Claim 8; Figure 8; 95pp; English.
CC Nucleic acids encoding mutant and wild type Axin and
CC oligonucleotides derived from them are useful for detecting
CC mutations in the Axin gene and for determining whether a subject is
CC likely to develop cancer (including breast, colorectal,
CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
CC type Axin and homologues of Axin are useful for treating subjects
CC who are likely to develop cancer (thyroid carcinomas). The nucleic
CC acids are also useful for diagnosing cancer and for detecting
CC molecules in cancerous cells. Wild type Axin, its antisense
CC molecule and identified compounds form pharmaceutical compositions
CC in the treatment of cancer. The compositions are also useful for
CC treating cancer by inhibiting tumorigenesis (by inducing degradation
CC of beta-catenin). The nucleic acid encoding Axin acts through
CC negative regulation of the Wnt pathway in the Nieuwkoop Center.
XX
SQ Sequence 992 AA:

Query Match 37.2%; Score 1655; DB 20; Length 992;
Best Local Similarity 42.7%; Pred. No.2.4e-128;
Matches 390; Conservativity 133; Mismatches 246; Indels 144; Gaps 30;

OY 12 DSSSFRBDAPPBPVGEERGE-----TPPCQPSV--GKVOSTRKMPVSSNARNEDGLG- 63
DB 12 dsssfredappbpvgeerge-----tppcqpsv--gkvostrkmpvssnarnedglg- 63
OY 64 EPEGRASPSPLTRMTKSLHSLGDDGAYLFRFLEREKCVDTLDFWACNGFROMNLK 123
DB 64 epegaspspltrmtkshslgddgaylfrflerekcvdtldfwacngfrotnlk 123
OY 200 EPEGASPSPLTRMTKSLHSLGDDGAYLFRFLEREKCVDTLDFWACNGFROMNLK 259
DB 200 epegaspspltrmtkshslgddgaylfrflerekcvdtldfwacngfrotnlk 259
OY 124 DT---KTLRVAKAIYKRYI-ENNSVSKOLKPKATKYIRIDGIKKOOIGSMFDOAOTEIO 179
DB 124 dt---ktlrvakaiykyri-ennsvskolkpkatkylridgikkgiigsmfdaqteiq 179
OY 260 dsnneekrlklatayrkyllidngivsrqtkpatsfkldcvmkqqlidpamfdqteiq 319
DB 260 dsnneekrlklatayrkyllidngivsrqtkpatsfkldcvmkqqlidpamfdqteiq 319
OY 180 AVMEENAVOFLTSIDYLEYVNSGGENTAYMNSGGLSKVLGCGYPTLNNEEEMTC- 236
DB 180 avmeenavofltsidyleyvrnsgeentaemngslgskvlcgypnlneeevctadik 236
OY 320 stmeentypsfklsdyleyrtgsgsprkvcsgsgtqgmsyuplclneedeewkcd 379
DB 320 stmeentypsfklsdyleyrtgsgsprkvcsgsgtqgmsyuplclneedeewkcd 379
OY 237 -----ADLKCKLSPTVVGSLSKTL-----RATASVSRSTETAEANGFRSRSDPVNVA 285
DB 237 -----adlkcklsptvvgslsktl-----ratasvrsstetaeangfrsrdpvnv 285
OY 380 qdadeddgrdplrps--rltkqlliletaaprsrtrnegreltygswr--epvnyyuv 435
DB 380 qdadeddgrdplrps--rltkqlliletaaprsrtrnegreltygswr--epvnyyuv 435
OY 286 GSGYVFAFATSANDSE---LSSDALTDMSMTSSVDGVPRYRMGSKKOLQREHMRSVK 342
DB 286 gsgyvfafatsandse---lssdaltdmsmtssvdgvprymgskkqlqremhmrsvk 342
OY 436 nsqyalapatsandseqqlssda---dlsltdssvdgippyrl--rghntremgesiq 490
DB 436 nsqyalapatsandseqqlssda---dlsltdssvdgippyrl--rghntremgesiq 490
OY 343 ANGQVSLPHFPTTRHRLPKEMTPVERPAFAAEELISRLKLEKLESHNSLEERLQOIREDE 402
DB 343 angovslphfpttrhrlpkemtpverpaafaellisrllekleshnsleerlqlrede 402
OY 491 vngvrplripriptympkrlr--vepqkfaeelhrleavgrtreaeekleerlkrymee 549
DB 491 vngvrplripriptympkrlr--vepqkfaeelhrleavgrtreaeekleerlkrymee 549
OY 403 EKEGSPQALSSRDGARVQVQRLALLPS-----GSYEEDPQTLDDHLSR 445
DB 403 ekegspqalssrdgarvqvqrlallps-----gsyeedpqtllddhlsr 445
OY 550 egedgemp---sgpmashkipsrpawhhfrpryvdmgsgjlrdaeenpeesldehvr 605
DB 550 egedgemp---sgpmashkipsrpawhhfrpryvdmgsgjlrdaeenpeesldehvr 605
OY 446 VLKTPCGQSPGVGRYSRSPSRPNHNNHNNHQQCHTLLSTGGLRPAACPLLG----- 500

```

Db 606 vmrtgpcspg-----pghrpsdsg-----vaktavlggtasgh 640
QY 501 -----KSFLEKQTT-----KHVHHYIHHNAVKTKEIEAATQRYVCLCGSDYCY 550
Db 641 gkhvpxlklkldtaglhhhrhvhnh-vhnsa-trkeqmaevavrrvgsfswgpetlgh 698
QY 551 SKCKSHPK-AREPL-PGEQFCGSRGGTLPRKNAKTEPGLALSARDGMSAAGPQLPG 608
Db 699 akprysenagtltsagdlpfvgktsapskrtlkkaesgkana-----evps 746
QY 609 --EEGDRSODVWQWMLSEERO---SKSKPHSQSIRKSYPLESAAACGERVSRHLLICA 663
Db 747 ltedaeknqkimgwlllegekeisrthkaghsaglrkqahessrplstierpgavhpwvs 806
QY 664 SGHSRVARAPFTQDPAMPPLTPPTLAQLEACRRLAEVSK-----POKORCCVASQ 718
Db 807 aqlrsvpsnlhfgdprmpnpapnplrtgleaarrrleeeekranklpskqrvyqavmq 866
QY 719 RDRHNSAAGAGASFPANP-----SLAPEDHKEPKKLASVHALQASELVVYTF 767
Db 867 r-----grtcvrcpacavrlsvvpavsdlelsetetksqtkaggsapcdslvgyyf 919
QY 768 CGEETPYRMLKAOSLTIGHFKEQLSKGNRYEKKASDEFACGAVPEETMDETVLP 827
Db 920 cgepiptlrvgravlrlgkelltkkgsyryyfkvdsdfcgvfveevredpevlrv 979
QY 828 YEGRIKVERID 840
Db 980 feekligvkevvd 992

```

RESULT 4
AAW96264
ID AAW96264 standard; Protein: 900 AA.
XX
AC AAW96264;
XX
DT 14-JUN-1999 (first entry)
XX
DE Human axlin.
XX

AXlin: Cancer: breast cancer; colorectal cancer;
KM gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
KM diagnosis: treatment; therapy; thyroid carcinoma; tumorigenesis;
KM beta-catenin.
XX
OS Homo sapiens.
XX
PN M09902179-A1.
XX
PD 21-JAN-1999.
XX
PF 09-JUL-1998; 98MO-US14414.
XX
PR 10-JUL-1997; 97US-0890865.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Constantlnl F, zeng L;
XX
DR WPI; 1999-120510/10.
XX
DR N-PSDB; AAX09012.
XX
PT Newly isolated nucleic acid encoding "axis inhibition" protein
XX (Axlin) - useful for detecting, diagnosing and treating cancer
XX
PS Disclosure: Figure 11, 95pp; English.
XX
CC Nucleic acids encoding mutant and wild type Axlin and
CC oligonucleotides derived from them are useful for detecting
CC mutations in the Axlin gene and for determining whether a subject is
CC likely to develop cancer (including breast, colorectal,

CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
CC type Axlin and homologues of Axlin are useful for treating subjects
CC who are likely to develop cancer (thyroid carcinomas). The nucleic
CC acids are also useful for diagnosing cancer and for detecting
CC mutations in cancerous cells. Wild type Axlin, its antisense
CC molecule and identified compounds form pharmaceutical compositions
CC in the treatment of cancer. The compositions are also useful for
CC treating cancer by inhibiting tumorigenesis (by inducing degradation
CC of beta-catenin). The nucleic acid encoding Axlin acts through
CC negative regulation of the Wnt pathway in the Nieuwkoop Center.
XX

Sequence 900 AA;

Query Match 36.1%; Score 1605; DB 20; Length 900;
Best Local Similarity 41.2%; Pred. No. 2,9e-124;
Matches 382; Conservative 125; Mismatches 248; Indels 172; Gaps 29;

```

QY 12 DPSSFRDAPRPVPGEGETPPCOPSVCKQSTKMPVS-----SN 54
Db 48 dlgsafedaprpvpggege-----lvtdeprpasyfscgkygikgetstat 97
QY 55 ARKNEDELG-EPGRASPDSPLTRWTSLSLSLGDQCAVLFRTFLREKCVDTLDFWA 113
Db 98 prrsdlldgyepgsasptpyllkwaeslnsllddggisifrtflkxgcadlldfwfa 157
QY 114 CNGFROMMLKDT--KTLRVAKAIYKRYI--ENNSVSKOLKPAKTYIRGIRKQOQGSV 169
Db 158 ctgfrklrlepcdsneekrlklaralyrkyllidnglvarqtkpackstfkiclmqllidpa 217
QY 170 MFDQATEIQAVMENAYOVFLSDIYLEYVSGGENTAVMS--NGSLGSLKVLGYLPT 227
Db 218 mfdqateiqatmeentypsflikedilyeytrtgsesprkcsdsgsgygyklsylypt 277
QY 228 LNEEEMTC-----ADLKCKLSPTVWGSLSTLRLATASVRETFAENCFRFR 276
Db 278 lneedeewkcdqdnedgdrdaaprrl-pqklllelaprvssrrysgretfygswr 335
QY 277 SDPVPNRYVSGVYFAPATSANDE--LSSDALTDMSMTQSVGVPPYRMRGSKOL 333
Db 336 -epnpyrvynaagyalapataandegsjsda---dtlsltdsvdglppryl--tkqh 389
QY 334 QREKHSVKANGOVSLPHFRTHRLPREMTVERPARAELISLEKIKLELSRHSLE 393
Db 390 rremgesaayngyvrphlprtyrvkevrv-vepqkfaeelhrlaeavqtrtaeeeklee 448
QY 394 RLOQIREDEKEGSEQLSSRDGAPV-----HPLALLS-----G 429
Db 449 rlrkrvmeege-----dgdpsgprpckklrppawhlfprlclwtacaglld 499
QY 430 SYEDPQTLDDHLRYLKTGCGOSPCVGRYSPRSRSPDHNNHNOCHTLSTSGK 489
Db 500 aheepneslidenhgvrlrtgrgspg-----pghrpsdsglv-----akm 540
QY 490 PVAACPLLGKSFLEKQTT-----HVNHHYIHHNAVKTKEIEAATQRYV 539
Db 541 pvalggaasghkhpksakldaaglhhrhvhnh--hstarkpqgeaaetrags 598
QY 540 LCPGCTDIYCYSK-----CSNHPKAREPLPGEQFCGSRGGTLPRKNAKTEPGLALSARD 594
Db 599 sfawglerphsagarsrgysesvgaapnasdglahsg-kyvackrtnakkaesgksast 655
QY 595 GGMSSAAGFPOLPG--EEGDRSODVWQWMLSEERO---SKSKPHSQSIRKSYPLESARA 649
Db 656 -----evrgaadeaknqkimgwlllegekeisrthrttgngssgtrkqpghenst 705
QY 650 APGERVSRHLLGASGHSRVARAPFTQDPAMPPLTPPTLAQLEACRRLAEVSK--- 706
Db 706 -----lslhwpagpqlrtsvpsnlhfgdprmpnpapnplrtgleaarrrleeeekrs 760
QY 707 --POKORCCVASQORBRNSAAGAGASFPANP-----SLAPEDHKEPKKLASV 753
Db 761 rapskgrvygevmt-----gracvrcpacavrlhvpavsdmelelsetrtsgtkvvgg 813

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AC AAY97154;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Murine regulator of G-protein signaling protein.
 XX
 KW RGS; regulators of G-protein signaling; GTPase activating protein; GAP;
 KW G-alpha protein; cell adhesion; chemotaxis; vulnerability; immunosuppressor;
 KW anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;
 KW cytoskeletal; hepatotropic; anti-anaemic; modulator; gene therapy.
 XX
 OS Mus sp.
 XX
 FH Key
 FT Domain
 FT Misc-difference 83 Location/Qualifiers
 FT Misc-difference 90 /note= "forms part of hydrophobic core"
 FT Misc-difference 100 /note= "forms part of hydrophobic core"
 FT Misc-difference 103 /note= "forms part of hydrophobic core"
 FT Misc-difference 104 /note= "forms part of hydrophobic core"
 FT Misc-difference 107 /note= "forms part of hydrophobic core"
 FT Misc-difference 109 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 111 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 112 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 115 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 116 /note= "forms part of hydrophobic core"
 FT Misc-difference 138 /note= "forms part of hydrophobic core"
 FT Misc-difference 139 /note= "forms part of hydrophobic core"
 FT Misc-difference 142 /note= "forms part of hydrophobic core"
 FT Misc-difference 143 /note= "forms part of hydrophobic core"
 FT Misc-difference 151 /note= "forms part of hydrophobic core"
 FT Misc-difference 152 /note= "forms part of hydrophobic core"
 FT Misc-difference 154 /note= "Makes direct contact with G-alpha-1"
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 FT Misc-difference 187 /note= "forms part of hydrophobic core"
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 FT Misc-difference 189 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 191 /note= "forms part of hydrophobic core"
 FT Misc-difference 192 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 193 /note= "forms part of hydrophobic core"
 FT Misc-difference 198 /note= "forms part of hydrophobic core"
 FT Misc-difference 198 /note= "forms part of hydrophobic core"
 PN WO200046236-A2.
 XX

PD 10-AUG-2000.
 XX
 PF 04-FEB-2000; 2000WO-US02977.
 XX
 PR 04-FEB-1999; 99US-0244314.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Hodge MR, Yowe D;
 XX
 DR WPI; 2000-532893/48.
 DR N-PSDB; AAA52090.
 XX
 PT Novel regulator of G-protein signaling nucleic acids and polypeptides,
 PT useful as diagnostic and investigative tools and to treat G-protein
 PT signaling disorders
 XX
 PS Claim 8; Page 104; 105pp; English.
 XX
 CC The RGS (regulators of G-protein signaling) protein genes, clones
 CC AAH16395 and m1975, were identified in human and murine spleen cDNA
 CC libraries, respectively. Both proteins have unique N- and C-terminal
 CC sequences. The C-terminal location of the RGS domain is consistent with
 CC RGSs known to act as GTPase activating proteins (GAPs) for G-alpha
 CC proteins. G-alpha-1 linked receptors support rapid adhesion and directed
 CC migration of leukocytes and other cell types. The novel RGS proteins may
 CC be used to modulate cell adhesion and chemotaxis, e.g. for aiding wound
 CC repair. The RGS proteins, related cDNAs and anti-RGS antibodies are
 CC useful for modulation, diagnosis and treatment of immune and respiratory
 CC disorders.
 XX
 SQ Sequence 235 AA;
 XX
 Query Match 4.3%; Score 193; DB 21; Length 235;
 Best Local Similarity 28.1%; Pred. No. 6,7e-08;
 Matches 50; Conservative 37; Mismatches 69; Indels 22; Gaps 5;
 QY 41 GKVOSTKPMVPSSNARRE-----DGLGE-----PGRASPSDPLRWTKSL 82
 DB 29 gkeetsleakirakekrnrlslilqprdfngetqasrallaketrvspeav-kwaesf 87
 QY 83 HSLGDDGAYLFPTFLEREKCVDTLDFEACNGFRQNLKDTLRVAKIYRYENN 142
 DB 88 dklshrdgvdafrflktfeesenlefwacedfkck-epqqlilkakayekfiqnd 146
 QY 143 SVSKQKLPAKTYIRQGIKQKQIGSVWFDAQRIEIQAVMEENAYOVLTSDILEV 200
 DB 147 apkevnldfnkeviakslagptlsh--fdtagrsvyqjmehsdykrltksetylhll 202
 XX
 RESULT 7
 ID AAB56929 standard; Protein: 220 AA.
 AC AAB56929;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1507.
 XX
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytoskeletal; cardiovascular; immunomodulatory; muscular;
 KW vulnerability; gastrointestinal; nephroretic; anti-infective; gynecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.
 XX
 OS Homo sapiens.
 OS
 XX
 PN WO200055174-A1.
 XX
 PD 21-SEP-2000.
 XX

[illegible]

FT		Signature"
FT	Region	58..177
FT	/note=	"RGF motif"
FT	Modified-site	8...11
FT	/note=	"Asn may be N-glycosylated"
FT	Modified-site	235..238
FT	/note=	"potential cAMP- and cGMP-dependent protein kinase phosphorylation site"
FT	Modified-site	11..14
FT	/note=	"potential casein kinase II phosphorylation site"
FT	Modified-site	66..69
FT	/note=	"potential casein kinase II phosphorylation site"
FT	Modified-site	220..223
FT	/note=	"potential casein kinase II phosphorylation site"
FT	Modified-site	93..95
FT	/note=	"potential protein kinase C phosphorylation site"
FT	Modified-site	97..99
FT	/note=	"potential protein kinase C phosphorylation site"
FT	Modified-site	161..164
FT	/note=	"potential protein kinase C phosphorylation site"
FT		
XX	M03844115-A2.	
XX		
XX	08-OCT-1998.	
PD		
XX	31-MAR-1998;	98WO-US06336.
PF		
XX	31-MAR-1997;	97US-0829110.
PR		
XX	(INCY-) INCYTE PHARM INC.	
PA		
PI	Goli SK, Hillman JL;	
P1		
DR	WPI; 1998-557112/47.	
N-PSDB;	AAV45442.	
PT	New regulators of G-protein signalling - useful for, e.g. diagnosis,	
PT	prevention and treatment of cancer and inflammation	
XX		
PS	Claim 19; Page 45; 65pp; English.	
XX		
CC	This is the amino acid sequence of a novel human regulator of	
CC	G-protein signalling, termed RGPS-2. It was deduced from a	
CC	consensus nucleic acid sequence (see AAV45442) derived from thymus	
CC	and other CDNA clones. RGPS-2 shares 46% and 37% identity with	
CC	human BL34 and RGS4, respectively. It shows significant	
CC	expression in inflamed, immortalised or cancerous cells and	
CC	tissues. The invention provides 2 regulators of G-protein	
CC	signalling, i.e. RGPS-2 and RGPS-1 (see AAW30560). The invention	
CC	also features nucleic acids encoding RGPS polypeptides,	
CC	oligonucleotides, peptide nucleic acids, fragments, portions or	
CC	antisense molecules, and expression vectors and host cells. It	
CC	also features antibodies specific for RGPS, and pharmaceutical	
CC	compositions comprising purified RGPS. It also provides methods	
CC	for stimulating cell proliferation using an RGPS or an agonist of	
CC	RGPS and for treating or preventing disorders (e.g. cancer)	
CC	associated with cell proliferation and inflammation using an	
CC	antagonist of RGPS.	
CC		
XX		
SQ	Sequence 243 AA:	
Query Match	3.8%; Score 170.5; DB 19; Length 243;	
Best Local Similarity	28.1%; Pred. No. 5.2e-06;	
Matches 55; Conservative 38; Mismatches 78; Indels 25; Gaps		

14 SSSFFEDARPPEEGETPPCOPSVGVOSTKPMPVSSNARNRNDGLGEPEGCRASP - 72

```
Db      49 shiftlae-----eaaglrasp-----edakp-----awrpsddhsdsgssssst 91
QY      73 ---SPLRRTKSLHSLIGDODGAVLFRFTLEERKCVDTLDFPACNGFROMNLKDTKTLR 129
Db      92 gskstakwaaslenlledpegvkrtrfllkfeeseenylfwlacedfkmgdk-lqmg 150
QY      130 VAKAIKRYIENNSVYSKQKPKATKYIRNDGIKQOIGSVMPDOATEIOAVMEENAYGV 189
Db      151 kakeiymtfl--sskassqvnvegsgsrlnleekleep-hplmfqkldqqlfnlmkydsysr 207
QY      190 FLRSDIYLEVRSRSGE 205
Db      208 flksdflfkhkrtee 223

RESULT  9
ID      AAM44834
AA      AAM44834 standard; peptide; 181 AA.
XX
AC      AAM44834;
XX
DT      21-JUL-1998 (first entry)
XX
DE      Human p26 protein.
XX
KW      Human; p26; brain; hybridisation; dephosphorylase inhibitory activity;
KW      probe; rat; haematogenesis.
XX
OS      Homo sapiens.
XX
PN      JP09299092-A.
XX
PD      25-NOV-1997.
XX
PF      26-DEC-1996; 96JP-0347877.
XX
PR      12-MAR-1996; 96JP-0055196.
XX
PA      (TAKE ) TAKEDA CHEM IND LTD.
XX
DR      WPI: 1998-056555/06.
XX
N-PSDB: AAV19304.
XX
PT      Mammalian p26 proteins and their related DNA - useful for screening
PT      for de-phosphorylase inhibitory compounds
XX
PS      Claim 1; Fig 2; 40pp; Japanese.
XX
CC      This amino acid sequence represents the human p26 protein. The encoding
CC      gene sequence was isolated from a human thymus cDNA library by phage
CC      plaque hybridisation using the rat p26 cDNA sequence (AAV19303) as a
CC      probe. The screening isolated the corresponding 889 bp sequence. p26
CC      protein is useful as a reagent for screening for compounds having
CC      dephosphorylase inhibitory activity. It is also useful as a treating and
CC      preventive agent for diseases related to the haematogenic system.
XX
SQ      Sequence 181 AA;

Query Match      3.8%; Score 168; DB 19; Length 181;
Best Local Similarity 28.6%; Pred. No. 5.3e-06;
Matches 44; Conservative 37; Mismatches 65; Indels 8; Gaps 4;

QY      56 RRNEDGGEPEGGRSPD-----SPLTRTKSLHSLIGDODGAVLFRFTLEERKCVDTLDFW 111
Db      12 krrpsddhsdsgssssshgskstakwaaslenlledpegvkrtrfllkfeeseenylfw 71
QY      112 FACNGFROMNLKDTKTLRVAKAIKRYIENNSVYSKQKPKATKYIRNDGIKQOIGSVWF 171
Db      72 lacedfkmgdk-lqmgkakeiymtfl--sskassqvnvegsgsrlnleekleep-hplmf 127
QY      172 DOAQTEIOAVMEENAYOVFLTSDIYLEVRSRSGE 205
```

```
Db      128 gklqqlfnlmkydsysrflksdflfkhkrtee 161

RESULT  10
ID      AAB54360
AA      AAB54360 standard; Protein; 207 AA.
XX
AC      AAB54360;
XX
DT      09-MAR-2001 (first entry)
XX
DE      Human pancreatic cancer antigen protein sequence SEQ ID NO:812.
XX
KW      Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
KW      detection; diagnosis; identification; cytostatic; neuroprotective;
KW      neurotropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KW      antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW      linkage analysis; tissue identification; tissue typing; forensic;
KW      neural; immune system; muscular; reproductive; gastrointestinal;
KW      pulmonary; cardiovascular; renal; proliferative.
XX
OS      Homo sapiens.
XX
PN      WO20005320-A1.
XX
PD      21-SEP-2000.
XX
PF      08-MAR-2000; 2000WO-0505989.
XX
PR      12-MAR-1999; 99US-0124270.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Rosen CA, Ruben SM;
DR      WPI: 2000-579444/54.
DR      N-PSDB: AAC99125.
XX
PT      New nucleic acid that is a pancreatic cancer antigen for preventing,
PT      treating, or ameliorating a medical condition, particular pancreatic
PT      cancer, or for use in assays for diagnosing a pathological condition -
XX
PS      Claim 11; Page 1267-1268; 1379pp; English.
XX
CC      AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC      proteins, called pancreatic cancer antigens, given in AAB54008 to
CC      AAB54466. The human pancreatic cancer antigens have cytostatic,
CC      neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,
CC      gynaecological, cardiant and antiinflammatory activities, and can be used
CC      in gene therapy. The polynucleotide and proteins can be used for
CC      preventing, treating, or ameliorating a medical condition or in assays
CC      for diagnosing a pathological condition or a susceptibility to one in a
CC      subject. Binding partners to the proteins and the activity of the
CC      proteins can be identified. The pancreatic cancer antigens can be used to
CC      detect, treat or prevent pancreatic disorders, especially cancer.
CC      Agonists and antagonists to the antigens can be screened for. The
CC      pancreatic cancer antigen polynucleotides can be used to design nucleic
CC      acid hybridisation probes that can be used in chromosome mapping, linkage
CC      analysis, tissue identification and/or typing and a variety of forensic
CC      and diagnostic methods. The proteins can be used to generate antibodies
CC      which are used to purify, detect and target the polypeptides, including
CC      both in vivo and in vitro diagnostic and therapeutic methods. The
CC      proteins can be used to treat or prevent neural, immune system, muscular,
CC      reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC      proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC      sequences used in the exemplification of the present invention.
XX
SQ      Sequence 207 AA;

Query Match      3.8%; Score 168; DB 21; Length 207;
Best Local Similarity 28.6%; Pred. No. 6.6e-06;
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 23, 2001, 11:01:57 ; Search time 14.92 Seconds

(without alignments)
1928.593 Million cell updates/sec

Title: US-09-587-574-1

Perfect score: 4445
1 MSSAVLVTLDPDPSSFRD.....DETVPWYEGRIKVERID 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4445	100.0	840	1 AXN2_MOUSE	088566 mus musculu
2	4310	97.0	838	1 AXN2_RAT	070240 ratius norv
3	4027.5	90.6	843	1 AXN2_HUMAN	Q9Y241 homo sapien
4	2632.5	59.2	812	1 AXN2_BRARE	P57095 brachydanio
5	1736	39.1	841	1 AXN2_CHICK	042400 gallus gall
6	1661	37.4	893	1 AXN1_RAT	020239 ratius norv
7	1655	37.2	992	1 AXN1_MOUSE	035625 mus musculu
8	1654.5	37.2	842	1 AXN1_XENLA	Q9Y9Y0 xenopus lae
9	1628	36.6	835	1 AXN1_HUMAN	P57094 brachydanio
10	1605	36.1	900	1 AXN1_HUMAN	015169 homo sapien
11	457.5	10.3	745	1 AXN1_MOUSE	09V407 dtrosophila
12	195	4.4	547	1 RGSE_MOUSE	P97492 mus musculu
13	190.5	4.3	544	1 RGSE_RAT	008773 ratius norv
14	189.5	4.3	519	1 RGSE_HUMAN	P49796 homo sapien
15	172.5	3.9	211	1 RGSE2_HUMAN	P41220 homo sapien
16	170.5	3.8	211	1 RGSE2_MOUSE	008849 mus musculu
17	167	3.8	167	1 RGSA_HUMAN	043665 homo sapien
18	164	3.7	180	1 RGSE_HUMAN	P57771 homo sapien
19	163	3.7	180	1 RGSE_RAT	P49804 ratius norv
20	161.5	3.6	216	1 GAIP_RAT	070521 ratius norv
21	159	3.6	181	1 RGSS_HUMAN	015539 homo sapien
22	159	3.6	181	1 RGSL_HUMAN	008116 homo sapien
23	157.5	3.5	205	1 RGSD_HUMAN	P49798 homo sapien
24	156.5	3.5	217	1 CAIP_HUMAN	P49799 homo sapien
25	154.5	3.5	181	1 RGSS_MOUSE	008850 mus musculu
26	154.5	3.5	205	1 RGSD_RAT	P49799 ratius norv
27	153	3.4	199	1 RGSG_BOVIN	046471 bos taurus
28	151.5	3.4	199	1 RGSG_RAT	P56700 ratius norv
29	151.5	3.4	205	1 RGSA_MOUSE	008899 mus musculu
30	151.5	3.4	1618	1 NEST_HUMAN	P48681 homo sapien
31	150.5	3.4	181	1 RGSS_RAT	P49800 ratius norv
32	149	3.4	159	1 RGSD_RAT	014921 homo sapien
33	149	3.4	2505	1 CCAA_HUMAN	000555 homo sapien

ALIGNMENTS

RESULT	1	AXN2_MOUSE	STANDARD	PRT	840 AA.
AC	088566: 090X16:				
DT	01-OCT-2000 (Rel. 40, Created)				
DT	01-OCT-2000 (Rel. 40, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)				
DE	(AXIL).				
GN	AXIN2.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96221239; PubMed=9554852;				
RA	Behrens J., Jerchow B.A., Wuerle M., Grimm J., Asbrand C.,				
RA	Wirtz R., Kuehl M., Wedlich D., Birchmeier W.;				
RT	"Functional interaction of an axin homolog, conductin, with beta-				
RT	catenin, APC, and GSK3beta."				
RL	Science 280:596-599(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,				
RA	Jenkins N.A., Warburton D., Constantini F.;				
RT	"Properties of mouse Axin2 and human AXIN2: chromosomal location,				
RT	expression pattern, interaction with Axin and effects on embryonic				
RT	axis formation."				
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.				
CC	- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES				
CC	BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-				
CC	CATENIN AND APC BY GSK-3B (BY SIMILARITY).				
CC	- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)				
CC	AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN				
CC	OCCURS VIA THE ARMD/ILDO REPEATS CONTAINED IN BETA-CATENIN.				
CC	TERMINAL COMPLEX (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).				
CC	- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY				
CC	PP2A (BY SIMILARITY).				
CC	- SIMILARITY: CONTAINS 1 RGS DOMAIN.				
CC	- SIMILARITY: CONTAINS 1 DIX DOMAIN.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; AF073788; AAC6047.1; -				095208 ovis aries
DR	EMBL; AF205889; AAF22800.1; -				015492 homo sapien
DR	MGI; MGI:1270862; Axin2.				P97428 mus musculu
DR	HSSP; P49799; IAGR.				P51823 homo sapien
DR	InterPro; IPR000342; -				014924 homo sapien
					09Y263 homo sapien
					Q18312 caenorhabdi
					P79348 bos taurus
					P29617 dtrosophila
					P46821 homo sapien
					Q14687 homo sapien
					003172 mus musculu

DR InterPro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PRINTS: PR01301; RGS-PROTEIN.
 DR PROSITE: PS50132; RGS; 1.
 KW Anti-oncogene: Phosphorylation.
 FT DOMAIN 81 200 RGS.
 FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 413 478 BETA-CATENIN BINDING SITE (BY SIMILARITY).
 FT DOMAIN 469 476 DIX.
 FT DOMAIN 758 840 POLY-HIS.
 FT CONFLICT 101 101 R -> K (IN REF. 2).
 FT CONFLICT 474 474 H -> Y (IN REF. 2).
 FT CONFLICT 484 503 S -> P (IN REF. 2).
 FT CONFLICT 503 503 F -> S (IN REF. 2).
 FT CONFLICT 603 603 G -> A (IN REF. 2).
 SQ SEQUENCE 840 AA: 92934 MW: A07D5F825DE7277 CRC64;

Query Match 100.0%; Score 4445; DB 1; Length 840;
 Best Local Similarity 100.0%; Pred. No. 9.9e-244;
 Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSAVLVTLDDPSSFFEDAPRRPVPEEGETPPCOPSVGVSTKPMVSNARRNED 60
 DB 1 MSSAVLVTLDDPSSFFEDAPRRPVPEEGETPPCOPSVGVSTKPMVSNARRNED 60
 QY 61 GLGPEGRASPDSPLTWTKSLHSLDGDQAVLFRFLEKEKCVDTLDFEACNGFROM 120
 DB 61 GLGPEGRASPDSPLTWTKSLHSLDGDQAVLFRFLEKEKCVDTLDFEACNGFROM 120
 QY 121 NLKTKTLRAKAIYKRIENNSVSKQLPATYTYRDIKIKOOIGSVMEFDAQTEIOA 180
 DB 121 NLKTKTLRAKAIYKRIENNSVSKQLPATYTYRDIKIKOOIGSVMEFDAQTEIOA 180
 QY 181 VMEENAOVELTSDIYLEYVRSAGENTAYMSGIGSLKVLGVLPTLNEEETCTADLK 240
 DB 181 VMEENAOVELTSDIYLEYVRSAGENTAYMSGIGSLKVLGVLPTLNEEETCTADLK 240
 QY 241 CKLSPTVVGSSKTLRAVASTETAEENGFRSEKRSDPVNPYHVSGYFAPATSANDS 300
 DB 241 CKLSPTVVGSSKTLRAVASTETAEENGFRSEKRSDPVNPYHVSGYFAPATSANDS 300
 QY 301 ELSSDALTDMSMTDSSVGVPRYRMSKKOLOREMHRSVKANGOVSLPHFRTHLPK 360
 DB 301 ELSSDALTDMSMTDSSVGVPRYRMSKKOLOREMHRSVKANGOVSLPHFRTHLPK 360
 QY 361 EMPVPEPAFAELISRLKLELESRHSLEERLQIREDEKEGSEQALSSRDGAPVQ 420
 DB 361 EMPVPEPAFAELISRLKLELESRHSLEERLQIREDEKEGSEQALSSRDGAPVQ 420
 QY 421 HPLALPSSGYEDPQTLIDHLSRYLKTGCGSPGVGRYSPPRSRSDNNHNNHQQCH 480
 DB 421 HPLALPSSGYEDPQTLIDHLSRYLKTGCGSPGVGRYSPPRSRSDNNHNNHQQCH 480
 QY 481 TLSTGGKLPVAVACPLLGSKSFLTKOTTKVHNHNTIHNNAVPTKEEIEAETOVNRC 540
 DB 481 TLSTGGKLPVAVACPLLGSKSFLTKOTTKVHNHNTIHNNAVPTKEEIEAETOVNRC 540
 QY 541 CPFGTGYCYCKSKSHKAPRLPGEOFCGSRGGLPKRNKSTEGALASADGMSA 600
 DB 541 CPFGTGYCYCKSKSHKAPRLPGEOFCGSRGGLPKRNKSTEGALASADGMSA 600
 QY 601 AGGPOLPGEGRSDQVWOMMESEKSKSPHSASQISKSYLEBARAPGGRVSRNHL 660
 DB 601 AGGPOLPGEGRSDQVWOMMESEKSKSPHSASQISKSYLEBARAPGGRVSRNHL 660
 QY 661 LGASGHSRVARAHPTQDPAHPPLTPNTLAQLEACRRLAEVSPQORCCVASQOQD 720
 DB 661 LGASGHSRVARAHPTQDPAHPPLTPNTLAQLEACRRLAEVSPQORCCVASQOQD 720
 QY 721 RNHSAAGAGASBPANSLAPEDHKPKKLASVHALQASELVVYFFCGEELPYRRMLKA 780

DB 721 RNHSAAGAGASBPANSLAPEDHKPKKLASVHALQASELVVYFFCGEELPYRRMLKA 780
 QY 781 QSLTLGHEKEQLSKKNRYRYFKKASDEFACGAFFEEIWMDETLYLPMWEGRIILKVERID 840
 DB 781 QSLTLGHEKEQLSKKNRYRYFKKASDEFACGAFFEEIWMDETLYLPMWEGRIILKVERID 840

RESULT 2
 ID AXN2_RAT STANDARD; PRT; 838 AA.
 AC 070240;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
 DE (AXIN).
 GN AXIN2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98226558; PubMed=9566905;
 RA Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M.,
 RA Kikuchi A.;
 RT "Axin, a member of the Axin family, interacts with both glycogen
 RT synthase kinase 3beta and beta-catenin and inhibits axis formation of
 RT Xenopus embryos.";
 RT Mol. Cell. Biol. 18:2867-2875(1998).
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
 CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
 CC OCCURS VIA THE AMADILLO REPEATS CONTAINED IN BETA-CATENIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS.
 CC -1- PPM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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 CC EMBL: AF017757; AAC40089.1; -
 DR HSPF, P49799; IACR.
 DR InterPro: IPR000342; -
 DR InterPro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PROSITE: PS50132; RGS; 1.
 KW Developmental protein; Phosphorylation.
 FT DOMAIN 81 200 RGS.
 FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 413 478 BETA-CATENIN BINDING SITE (BY SIMILARITY).
 FT DOMAIN 469 474 POLY-HIS.
 FT DOMAIN 756 838 DIX.
 SQ SEQUENCE 838 AA: 92947 MW: 45B825C13BA07F37 CRC64;

Query Match 97.0%; Score 4310; DB 1; Length 838;
 Best Local Similarity 96.9%; Pred. No. 4.1e-236;

Matches 814; Conservative 7; Mismatches 17; Indels 2; Gaps 1;

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OY 1 MSSAVLYTLPPSSSFREDAPRPVPGEGETPPCQPSVGVOSTKRPVSSNARRND 60
Db 1 MSSAVLYTLPPSSSFREDAPRPVPGEGETPPCQPSVGVOSTKRPVSSNARRND 60
OY 61 GLGEPEGASPDSPLTRTKSLHSLGDODGAYLFRFLEKREKCVDTLDFWACNGFROM 120
Db 61 GLGEPEGASPDSPLTRTKSLHSLGDODGAYLFRFLEKREKCVDTLDFWACNGFROM 120
OY 121 NLKDTKTLRAKAIYKRIENNSVSKOLKPKATKYINDGKIKQOIGSVMDQATEIOA 180
Db 121 NLKDTKTLRAKAIYKRIENNSVSKOLKPKATKYINDGKIKQOIGSVMDQATEIOA 180
OY 181 VMEBAVAVFLTSDIYLYEVRSRGENTAYMNGSLKVLGCTPLTNEEDMTCADLK 240
Db 181 VMEBAVAVFLTSDIYLYEVRSRGENTAYMNGSLKVLGCTPLTNEEDMTCADLK 240
OY 241 CKLSPTVVGSLSKTLRATASVSTETAEENGFRKSPDPVNPYHVGSGYVAPATSANDS 300
Db 241 CKLSPTVVGSLSKTLRATASVSTETAEENGFRKSPDPVNPYHVGSGYVAPATSANDS 300
OY 301 ELSDALTDSDSMSTDDSVGVPRYRMGSKOLOREMHRSYKANGOVSLPHRPTRHLPK 360
Db 301 ELSDALTDSDSMSTDDSVGVPRYRMGSKOLOREMHRSYKANGOVSLPHRPTRHLPK 360
OY 361 EMTPEPAFAFAELISRLKLELESHSLLEERLOQIREDEKSGSDALSSRGCARVQ 420
Db 361 EMTPEPAFAFAELISRLKLELESHSLLEERLOQIREDEKSGSDALSSRGCARVQ 420
OY 421 HPLALLPGSGVEEDPQTLIDHLSRVLTQPCQSPGVGYSRSRSPDHNNHNNHQQH 480
Db 421 HPLALLPGSGVEEDPQTLIDHLSRVLTQPCQSPGVGYSRSRSPDHNNHNNHQQH 480
OY 481 TLLSTGSKLPRVACPLLGSKSLTKQTQTKVHNHYIHNNHNAVPKTELEAATORVCL 540
Db 481 TLLSTGSKLPRVACPLLGSKSLTKQTQTKVHNHYIHNNHNAVPKTELEAATORVCL 540
OY 541 CRGCGDYCYCKSKSHRPARERLPGEORCGSGTLPRKNACTGRCALSRDGMSSA 600
Db 541 CRGCGDYCYCKSKSHRPARERLPGEORCGSGTLPRKNACTGRCALSRDGMSSA 600
OY 601 AGGPOLPEEGDRSDVQWQMLSESRQSKSPHSAQSIIRKSYLESARAPGERVSRNHL 660
Db 601 AGGPOLPEEGDRSDVQWQMLSESRQSKSPHSAQSIIRKSYLESARAPGERVSRNHL 660
OY 659 AGAPQLPEEGDRSDVQWQMLSESRQSKSPHSAQSIIRKSYLESARAPGERVSRNHL 658
Db 659 AGAPQLPEEGDRSDVQWQMLSESRQSKSPHSAQSIIRKSYLESARAPGERVSRNHL 658
OY 721 RHHSAAGAGASPRANPSLAPEDHKEPKKLASVHALQASELYVTFEGCEELPYRMKLK 780
Db 721 RHHSAAGAGASPRANPSLAPEDHKEPKKLASVHALQASELYVTFEGCEELPYRMKLK 780
OY 719 RHHPRATGAGPTSFSPNPSLASEDHKEPKKLASVHALQASELYVTFEGCEELPYRMKLK 778
Db 719 RHHPRATGAGPTSFSPNPSLASEDHKEPKKLASVHALQASELYVTFEGCEELPYRMKLK 778
OY 781 OSLTGHKREOLSKKGNRYFYFKKASDFACAVFEEDVTVPMYBGRITLQKERTD 840
Db 781 OSLTGHKREOLSKKGNRYFYFKKASDFACAVFEEDVTVPMYBGRITLQKERTD 840
OY 779 OSLTGHKREOLSKKGNRYFYFKKASDFACAVFEEDVTVPMYBGRITLQKERTD 838
Db 779 OSLTGHKREOLSKKGNRYFYFKKASDFACAVFEEDVTVPMYBGRITLQKERTD 838

```

RESULT 3
AXN2_HUMAN
ID AXN2_HUMAN STANDARD: PRT: 843 AA.

AC 091211: Q9UH84;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
DE (AXIL).
CN AXIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxId=9606;

Query Match 90.6%; Score 4027.5; DB 1; Length 843;
Best Local Similarity 89.7%; Pred. No. 3.6e-220;
Matches 758; Conservative 31; Mismatches 49; Indels 7; Gaps 3;

```

OY 1 MSSAVLYTLPPSSSFREDAPRPVPGEGETPPCQPSVGVOSTKRPVSSNARRND 60
Db 1 MSSAVLYTLPPSSSFREDAPRPVPGEGETPPCQPSVGVOSTKRPVSSNARRND 60
OY 61 GLGEPEGASPDSPLTRTKSLHSLGDODGAYLFRFLEKREKCVDTLDFWACNGFROM 120
Db 61 GLGEPEGASPDSPLTRTKSLHSLGDODGAYLFRFLEKREKCVDTLDFWACNGFROM 120

```

[1]
SEQUENCE FROM N.A.
RA MEDLINE-99168905; PubMed-10049590;
RA Mai M., Qian C., Yokomizo A., Smith D.I., Liu W.,
RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
RT chromosome 17q23-q24."
RL Genomics 55:341-344(1999).
[2]
SEQUENCE FROM N.A.
RC Tissue-Brain, and Lymphoblast;
RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
RA Jenkins N.A., Warburton D., Constantini F.,
RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
RT expression pattern, interaction with Axin and effects on embryonic
RT axis formation."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).
CC - SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TERNARY COMPLEX (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: CYTOPLASMIC.
CC - TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.
CC - PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC - SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC - SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC
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DR EMBL: AF078165; AAD20976.1; -;
DR EMBL: AF205888; AAF22799.1; -;
DR MIM: 604025; -;
DR InterPro: IPR000342; -;
DR InterPro: IPR001158; -;
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PRINTS: PR01301; RGS/PROTEIN.
DR PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
DR DOMAIN 81 200
FT DOMAIN 327 413
FT DOMAIN 413 476
FT DOMAIN 469 474
FT DOMAIN 761 843
FT CONFLICT 37 62
FT CONFLICT 346 346
FT CONFLICT 572 636
FT CONFLICT 687 687
FT CONFLICT 696 696
FT SEQUENCE 843 AA; 93557 MW; F7B62BED6A4664D CRC64;

```

Db 61 GLEBGRASPSPLRTMTKSLHSLGDODGAYLFRFLEREKCVDTLDFWACNGFRM 120
Oy 121 NLKDTKTLRAKAIYKRYIENNSVSKOLKPAKTYIPDGIKKOQIGSMFOAQEIOA 180
Db 121 NLKDTKTLRAKAIYKRYIENNSVSKOLKPAKTYIPDGIKKOQIGSMFOAQEIOA 180
Oy 181 VMEENAYOVFLTSDIYLEVRSNGENTAYMSNGISLVLGCLPTLNEEBEWTCAJL 240
Db 181 VMEENAYOVFLTSDIYLEVRSNGENTAYMSNGISLVLGCLPTLNEEBEWTCAJL 240
Oy 241 CKLSPTVGLSKTLRATASVSTEAENGFRSFRKSDPVNRYHNGSGYVAPATISANDS 300
Db 241 CKLSPTVGLSKTLRATASVSTEAENGFRSFRKSDPVNRYHNGSGYVAPATISANDS 300
Oy 301 ELSSDALTDSDMSMTDSSVDGVPYRMGSKKOLQREMHRSYKANGOVSLPHFPTHTLPK 360
Db 301 ELSSDALTDSDMSMTDSSVDGVPYRMGSKKOLQREMHRSYKANGOVSLPHFPTHTLPK 360
Oy 361 EMTPEPAFAAELISRLKLEKLESHSLERLQOIREDDEKSGEQALSRRDGAPO 420
Db 361 EMTPEPAFAAELISRLKLEKLESHSLERLQOIREDDEKSGEQALSRRDGAPO 420
Oy 421 HPLALLPSGSYEEDPOTLIDHLSRVLTGPGQSPGVGRSPRSRPHHHHNOCH 480
Db 421 HPLALLPSGSYEEDPOTLIDHLSRVLTGPGQSPGVGRSPRSRPHHHHNOCH 480
Oy 481 TLSTGKLPVVA----ACPLIGKSFLLKQTKHVNHHYIHHNAVPKTEIEAATOR 536
Db 481 TLSTGKLPVVA----ACPLIGKSFLLKQTKHVNHHYIHHNAVPKTEIEAATOR 536
Oy 537 VRCLEPGGDDYCYCKSKSHPARPRLPDEQRCGRSTLKRNAKGTPEGLASAROGG 596
Db 537 VRCLEPGGDDYCYCKSKSHPARPRLPDEQRCGRSTLKRNAKGTPEGLASAROGG 596
Oy 597 MSSAGGQPLDEEGDRSQDWOMWLESEKSKSPHSAQISIRKSYPLESARAAGEVVS 656
Db 597 MSSAGGQPLDEEGDRSQDWOMWLESEKSKSPHSAQISIRKSYPLESARAAGEVVS 656
Oy 657 RHHLIGA-SGHSRSVAAHNPFTODPAMPRLPPTNTLAOLEBACRRLAEVSKPOROCVA 715
Db 657 RHHLIGA-SGHSRSVAAHNPFTODPAMPRLPPTNTLAOLEBACRRLAEVSKPOROCVA 715
Oy 716 SQQRDRNHSAGQAGASFPANPSLAPEDHKPKKLASVHNAQASELVYTFPGCEELPYR 775
Db 716 SQQRDRNHSAGQAGASFPANPSLAPEDHKPKKLASVHNAQASELVYTFPGCEELPYR 775
Oy 776 RMLKAQSLTLGHFEQJLSKGNRYRYFKKASDEFACGAVEIWDDEVLPYMYGRIILGK 835
Db 776 RMLKAQSLTLGHFEQJLSKGNRYRYFKKASDEFACGAVEIWDDEVLPYMYGRIILGK 835
Oy 836 VERID 840
Db 836 VERID 843

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RA Bae Y.-K., Hibi M., Hirano T.:
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
RT formation of the dorsal organizer in zebrafish."
RL Mech. Dev. 91:293-303(2000).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEIN AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB032263; BA092440.1; -.
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -.
DR InterPro: IPR001158; -.
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PSS0132; RGS; 1.
DR Developmental protein: Phosphorylation.
KW DOMAIN 84
KW DOMAIN 203
FT DOMAIN 329
FT DOMAIN 415
FT DOMAIN 415
FT DOMAIN 467
FT DOMAIN 412
FT DOMAIN 419
FT DOMAIN 730
FT DOMAIN 812
SQ SEQUENCE 812 AA; 91496 MW; 4655ADA6DE2240CC CRC64;

Query Match 59.2%; Score 2632.5; DB 1; Length 812;
Best Local Similarity 62.1%; Pred. No. 1,8e-141;
Matches 535; Conservative 88; Mismatches 154; Indels 85; Gaps 15;

Oy 10 LPDPS-SFREDAPRPVPEGEDETPCQPSVGKOSTKPM-PVS-----SNRRNE 59
Db 5 LTPDPSVSEFREDAPRPVPEGEDETPCHPS--KLAMMRKQDVKTIIMDLRSTARRBE 62
Oy 60 DGLGEPRGRASPSPLRTMTKSLHSLGDODGAYLFRFLEREKCVDTLDFWACNGFRQ 119
Db 63 DGLGEPRGRASPSPLRTMTKSLHSLGDODGAYLFRFLEREKCVDTLDFWACNGFRQ 122
Oy 120 MNLKDTKTLRAKAIYKRYIENNSVSKOLKPAKTYIPDGIKKOQIGSMFOAQEIOA 179
Db 123 MNLKDTKTLRAKAIYKRYIENNSVSKOLKPAKTYIPDGIKKOQIGSMFOAQEIOA 182
Oy 180 VMEENAYOVFLTSDIYLEVRSNGENTAYMSNGISLVLGCLPTLNEEBEWTCAJL 239
Db 183 VMEENAYOVFLTSDIYLEVRSNGENTAYMSNGISLVLGCLPTLNEEBEWTCAJL 242
Oy 240 CKLSPTVGLSKTLRATASVSTEAENGFRSFRKSDPVNRYHNGSGYVAPATISAND 299
Db 243 KAKALATVVGLSAKTIR-SPLRAVADALKGYRSTRSPGNPNRTSGVSPAPATISAND 301
Oy 300 ELSSDALTDSDMSMTDSSVDGVPYRMGSKKOLQREMHRSYKANGOVSLPHFPTHTLP 359
Db 302 SEVSDALTDSDMSMTDSSVDGVPYRMGSKKOLQREMHRSYKANGOVSLPHFPTHTLP 361
Oy 360 KEMTPPEPAFAAELISRLKLEKLESHSLERLQOIREDDEKSGEQALSRRDGAPO 419
Db 362 KEMTPPEPAFAAELISRLKLEKLESHSLERLQOIREDDEKSGEQALSRRDGAPO 416
Oy 420 HPLALLPSGSYEEDPOTLIDHLSRVLTGPGQSPGVGRSPRSRPHHHHNOCH 479
Db 417 HPLALLPSGSYEEDPOTLIDHLSRVLTGPGQSPGVGRSPRSRPHHHHNOCH 468

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OY 769 GEEIPRRMLKASQSLTGHFKESLKKGNRYRYFKKASDEFCAGVFEEMDETVLPMY 828
DB 770 GSEIPRFLVKGRRVVLGQFKELTKKGNRYRYFKKASDEFCAGVFEEMDETVLPMY 829
OY 829 EGRIIGKVERID 840
DB 830 EKIIGKVERID 841

RESULT 6
AXNI_RAT
ID AXNI_RAT STANDARD. PRT: 893 AA.
AC 070239:
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE AXIN 1 PROTEIN (AXIS INHIBITION PROTEIN 1) (RAXIN) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain:
RX MEDLINE=98151361; PubMed=9482734;
RA Ikeda S., Kishida S., Yamamoto H., Murali H., Koyama S., Kikuchi A.;
RT Axin, a negative regulator of the Wnt signaling pathway, forms a
RT dependent phosphorylation of beta-catenin.
RL EMO J. 17:1371-1384(1998).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS
CC PLAKOGLOBIN (GAMMA-CATENIN). APC, DVL AND PPA (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOSOL; PLASMA MEMBRANE (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG
CC FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,
CC SPLEEN AND LIVER.
CC -1- PPM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PPA (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: AF017756; AAC40066.1; ALT_INT.
DB HSSP: P49799; IAGR.
DB InterPro: IPR000342;
DB InterPro: IPR001158;
DB Pfam: PF00615; RGS; 1.
DB Pfam: PF00778; DIX; 1.
DB PROSITE: PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT NON_TER 1
FT DOMAIN 154 277 RGS.
FT DOMAIN 414 498 GSK-3B BINDING SITE.
FT DOMAIN 499 567 BETA-CATENIN BINDING SITE.
FT DOMAIN 811 893 DIX.
SQ SEQUENCE 893 AA; 99188 MW; 3CCBD224EDD384C CRC64;

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Query Match

37.4%; Score 1661; DB 1; Length 893;

```

Best Local Similarity 42.6%; Pred. No. 1,4e-86;
Matches 382; Conservative 136; Mismatches 231; Indels 148; Gaps 28;

OY 12 DPSSSFREDAPRPVPEGE-----TPPCPSV--GKQSTKPMYSSNRNRNDIG- 63
DB 77 DLGASFTEDAPRPVPEGEGLVSTDSRPVNHSCSGKSTIKETSTATPRRDLGLY 136
OY 64 EPEGASPDSPLTRWTKSLHSLDQDCAVLFERFLEKCVDTLDPFACNGFRQMLK 123
DB 137 EPEGASPTPYLWAEHSLDQDGLSLFRFLQECGADLDWFACSGFRKLEPC 196
OY 124 DT---KTLRVAIKYKRI--ENNSVSKOLKPKATKTYRDIKROQGVFDDAQTETQ 179
DB 197 DSNEKRLKLARILRYKTYLDSNGIVSRQTKPAKSTIKOCVMQOQDPAFDDAQTETQ 256
OY 180 AVDEBNAYOVFLSDIYLEVYRSGGENTAYWS--NGIGSLKYLGYLPTLNEEEMTC- 236
DB 257 STMEENTYPSFLKSDIYLETRTSESPKVCSDSSSGSGKGMGYLPTLNEDEMKCD 316
OY 237 ----ADLCKLSPYVGLSEKTL-----RATVSVSTEAENGFRSPRPVNPYHY 285
DB 317 QDADEDDGRDSVPS--RLTKLLETAAPRAAPSRRYNGRELRTGSMR--EPVNPYV 372
OY 286 GSGYVPAFATSSANDSE--LSSDALTDMSKMTDSVGVPPYRMGSKLOREMRSVK 342
DB 373 NSGYALAPATSSANDSEQSSLSDA--DTLSTDSSVDGIPIRYI--RKQRRREMESVQ 427
OY 343 ANGVSLPHFRPHRYRLKEMTPVPRAPAFADLLSLKLEKLESLRSLSEERLOQREDE 402
DB 428 VNGVNPRLPHRYRMYKELR--VEQCFABELLHRLVAVGTREAEKLEERLRMYER 486
OY 403 EKEGSEQALSSRDGAPVNDPLALPS-----GSYEEDPQTLDHLSR 445
DB 487 EGEDGEWP-----SGPMASHKLPSVAPMHNHPRRYVDMCGGLDADHENEGLDDEHYR 542
OY 446 VLTPPGQSGVGVYRSPRSRPHNNHNNHQQCHTLTSGKLPVYACPLIG- 500
DB 543 VMTRPGQSG- - - - -PGHRSPPDSGH-----VAKTAVLGGTASGH 577
OY 501 ----KSFLLKQTT-----KVNHNHYIHNHAPVPTKEETEAETORVRLCPGGTDYCY 550
DB 578 GKAPKLGKLDAGLHNHNVHN--VHNNSA--RPEQMDAEARVQSSFSMGPRTGH 635
OY 551 SKCKSHPKA--PEPLDEGDFGSGRGTLPKRNKAGTEPGLASARDGMSAAGFOLPG 608
DB 636 AKPRSYSESTGTNPASGDLAFGGKASAPSKRNTKKAESGMNSA-----EYVS 683
OY 609 --EGRSDVWQWMLSEBRO--SKSRHSAQSTIKSTPLSARAAPGERVSRHHLGA 663
DB 684 TTDAKKNQKIMQWITEGEKLSRHRKAGHSGGMKQDAHSSRPLSTERGAVHPVWS 743
OY 664 SGHSRSVARNHPTODPAMPPLTPPNTLAQLEACHRLAEVSKPKQRCQVSAQOORNH 723
DB 744 AQLRNSVQSHLFIQDPMPNAPRPLQLDEARRRLDEEKRANK--LPSKORTSQ 800
OY 724 SAAGGAGAPNPANPSLAPBDHKEPKKLASVALQSELVYVTFCCGEELPYRMLKASL 783
DB 801 KRAGGSAPP-----CDSIVAVYFPGCEPIRYPTLVGRVAV 836
OY 784 TLGHFKESLKKGNRYRYFKKASDEFCAGVFEEMDETVLPMDEGRIGKVERID 840
DB 837 TLGQRELLTKKGSYRYFYFKKASDEFCAGVFEEMDETVLPMDEGRIGKVERID 893

RESULT 7
AXNI_MOUSE
ID AXNI_MOUSE STANDARD. PRT: 992 AA.
AC 035625:
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT).
GN AXIN1 OR AXIN OR FU.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA MEDLINE=9373830; Pubmed=9230313.
RX Zeng L., Fagotto F., Zhang T., Hsu W., Vasicsek T.J., Perry W.L. III,
RA Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMD/BD0 REPEATS
CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
CC PLAKOGLOBIN (GAMMA-CATENIN), APC, DVL AND PR2A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOSOL; PLASMA MEMBRANE (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY.
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PR2A.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
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CC -----
DR EMBL: AF009011; AAC53285.1; -.
DR HSSP: P49799; IAGR.
DR MGD: MGI:1096327; Axin.
DR InterPro: IPR000342; -.
DR InterPro: IPR001158; -.
DR Pfam: PF00615; RGS. 1.
DR Pfam: PF00778; DIX. 1.
DR PROSITE: PS50132; RGS. 1.
KW Developmental protein; Phosphorylation; Alternative splicing.
FT NON_TER 1
FT DOMAIN 10 18 POLY-ALA.
FT DOMAIN 217 340 RGS.
FT DOMAIN 477 561 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 562 630 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DOMAIN 910 992 DIX.
FT VASAPLIC 860 895 MISSING (IN ISOFORM 2).
SO SEQUENCE 992 AA; 109917 MW; 70EBB53D387BD26F CRC64;

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Query Match 37.2% Score 1655; DB 1: Length 992;
Best Local Similarity 42.7% Pred. No. 3.4e-86;
Matches 390; Conservative 133; Mismatches 246; Indels 144; Gaps 30;

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OY 12 DPSSSFREDARPPVPEGE-----TPCQPSV--GKVSQKRPVSSNARNRNDGLG- 63
DB 140 DLGASFTDARPPVPEGEGLVSTDSRPVNHSPGSGKSTSTKSTSTATPRKSLDLG 199
DB 64 EPEGASPDSPULRWTKSLHSLDGDGAVLFRFLEREKCVDTLDFWACNGFRQMLK 123
DB 200 EPEGASPTPYLRWASLSHSLDDQGISLFRFLKQEGCADDLDFWACSGFRKLEPC 259
OY 124 DT---KTLRAVAKATYKRTI-ENNSVVSQQLAPATYTIKDGKKQOIGSVMDQATQ 179
DB 260 DSNERRKLKALRYKRYLDSNGISVROTQPKATSKFTKDCVMKQOIDPAMDQATQ 319

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OY 180 AVMEENAYQVFLTSDIYLEYVRSSGGEENTAYMS--NGGLSGKVLGGLYPTLNEEEMTC- 236
DB 320 STMENBTIPSLKSDIYLETYRTGSESPKVCSDSGSGTGKMGGLYPTLNEDEEMKCD 379
OY 237 -----ADLKSLPTVVLGSSKTL-----RATASVSTETAEENFRRFSKSDPVPNRYH 285
DB 380 QDADDDCRODLPSPS--RLTQKLLLETAAPAPSSRRYNEGELLYGSMR--EPNPNRYV 435
OY 286 GSGVFPAPATGANDSE---LSSDALTDMSKMTDSSVDCVPPRYMGSKKOLQREHNSVK 342
DB 436 NSGVLPATPATSANDSEQDLSDA---DTLSLTDSSVGVGIPRYRI--RKQHNREMEISIO 490
OY 343 ANGVSLPHFRPHTNRLKREMPVPERAFAELISLTKLELSEHNSLEPRLOIRDE 402
DB 491 VNGRPLPHIRPTTYMPKEIR-VEROKFAEELIHLEAVQRTREKEELEERLAKVRME 549
OY 403 EKEGSEQALSSRDGAPVONPLALPS-----GSYEEDPOTIILDHLSR 445
DB 550 EGEDEEMP-----SGFMASHKLPYRAMNHPRRYVDMGCSGLRANHNEPESILDEHYOR 605
OY 446 VLKTPGCSQPGVGRISPSKRSRPNHNNQOCHTLSTGSKLPVVAACPLGG----- 500
DB 606 VMKTPGCSQPG-----PGRHSPDSGH-----VAKTAVLGSTASGH 640
OY 501 -----KSLFTQQT-----KHVNHVYINNAVYKTELEAATQVRCLCGSTDYCY 550
DB 641 GKNVPRKLGKLDLTAGLNNHNNHNNH--VHNSA--RKEOMEAEVARRVOSSPSMGETIGH 698
OY 551 SKCKSHPK-ABEPL-RGBOFCGSRGCTLYKRNKSTERGLALSARDGMSAAGSPOLPG 608
DB 699 AKPRYSYNAGTTLAAGDLRFGCKTSAPSKRYTKKAESGKNANA-----EVP 746
OY 609 --EEDRSQDWMQMLSEBRO---SKSRPHASQSTIRKTPLESAAAGGERVSRHNLGA 663
DB 747 TTEDEKQOKMOWIEEKEKELSRHKAHGSSGLRQQAQANSSRLSTIERGAVNPNWS 806
OY 664 SGHSRSVARNHPFTQDPMPRLTPNPTLAQLEAEACRYLAEVSK-----POKORCVASQ 718
DB 807 AQLRNSVQPSHLFIODPLMPRPAPNPLQLDEARRRLEEEKRANKLPKSKRYVQAVNQ 866
OY 719 RDRNHSAGQACASPFANP-----SLAPDHEKPKKLASVHALQASELVVYTF 767
DB 867 R-----GRICVPACAPVLSVVPVAVSDLESETETKSQRKAGGSAPPCDSIVGYGF 919
OY 768 CGEELPYRMLKAOSLTGHEKEOLSKKGNRYRYKKKASDERACGAVPEIIDDDETLPM 827
DB 920 CGEPLPYRVLVNGRAVTLGQFKELLTKKGSYRYRKVSDERFCGVPEVEVREDEVLV 979
OY 828 YEGRIIGKVERID 840
DB 980 PEEKIIGKVERKD 992

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RESULT 8
AXN_XENLA STANDARD; PRT; 842 AA.
ID AXN_XENLA
AC 09YGYO;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN) (XAXIN).
GN AXIN OR AXN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99173782; Pubmed=10072781.
RA Hedgepeth C.M., Deardorff M.A., Klein P.S.;
RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
expressed in the anterior midbrain.";

```

RL Mech. Dev. 80:147-151(1999).
 CC - FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC - DEVELOPMENTAL STAGE: WEAKLY AND UBQUITOUSLY EXPRESSED THROUGHOUT
 CC MESENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.
 CC - PFM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC - SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC - SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -----
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 CC -----
 DR EMBL: AF097313; AAC71036.1; -
 DR HSSP: P49799; IAGR.
 DR InterPro: IPR000342; -
 DR InterPro: IPR001158; -
 DR Pfam: PF00778; DIX; 1.
 DR Pfam: PF00615; RGS; 1.
 DR PROSITE: PS0132; RGS; 1.
 DR Developmental protein; Phosphorylation.
 FT DOMAIN 88 211 RGS.
 FT DOMAIN 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
 FT SIMILARITY).
 FT DOMAIN 760 842 DIX.
 FT SEQUENCE 842 AA; 94459 MW; BDA152734C97191E CRC64;
 Query Match 37.28; Score 1654.5; DB 1; Length 842;
 Best Local Similarity 42.58; Pred. No. 3e-86;
 Matches 385; Conservative 125; Mismatches 246; Indels 149; Gaps 28;
 QY 12 DPSSFFEDAPRPVPEEGE--TPPCOPSVGKOSTKPMV-----SSNARRRDEGLG- 63
 DB 11 DLGSGFEDAPRPVPEEGELITTDQRPSTHTYSLKNDGKIKMETSTARRRDLGLG 70
 QY 64 EPERASPDPLRTWTSLSHSLDODGAYLFTTLEKRCVDTLDFWACNGFRQMLK 123
 DB 71 EPEGSASPTPYLKWASLSHSLDDODGHLFTFTLQDNCADLLDFWACSGFRKLEPN 130
 QY 124 DTKT---LRVAKATYKRYI-ENNSVSKOLKPAKTKYIRGDIKKQOIGSWFQDAQTEIQ 179
 DB 131 DSKYERKLAKAKIKKYVLDNSGIYSKQIKPATKSTIKCVLRQOQIDPAMFQDAQTEIQ 190
 QY 180 AVMEENAYQVLTSDIYLEVRSRGENTAYMS--NGSLGSLKYLGLPLTNEEEEMTC- 236
 DB 191 SMEDNTYPVFLKSDIYLETGTGGESPKNYVSSQSSSGTKGKPSGLPLTNDDEMRCD 250
 QY 237 -----ADLKC--KLSPTVYGLSKTLRTAYASTETAENCFRSPKRSDPVNPYVGS 287
 DB 251 QGGEHERERCIPSSLSFQKRLADSSHCAGSNRRLSDGRE--FRPGTWREPNPYVNT 308
 QY 288 GYVFAPATYSANDE--LSSDALTDSSMTDSSVDGVPYRMGSKQOLQREHRSVKAN 344
 DB 309 GYVAGAVTANSDEQSSMSDA---DTMSLTDSVDCIPIYRL--RKHYRREQESANAN 363
 QY 345 GOVSLPHFPTHTRLPKEMTPVEPAFAELISRLKLELESRHSLEERLQOIREDEK 404
 DB 364 GRPLPLHIRTGYHMPKDI-HVDEKFAELISRLLEVLRDREKQLERIKRVARE-- 420
 QY 405 EGSEQALSSRDGAPVQHPLALLPSG-----SYEDPQTLTDH 442
 DB 421 EGDGDGVSSGSPV-ISHK---LPSGPMHMFNSRYSETGCVGQIIRDAHEENPESITLDEH 476

QY 443 LSRVLKTPGCOSSPGYGRYSRSPDHHQ-----HHHQOCHTLSTGGKL 489
 DB 477 VQRVKTKGCOSSPGGRSPKSRSDGHLSTLPGLCTMOTGKHSKSTAKVDSGNL 536
 QY 490 PVVACPILGSKFELTKOTYHNNHYTHNNAVPTKEIEAEATORYRCCLCPGDTYYC 549
 DB 537 -----HHHKVYHN-VHNIQYKPKQIDIGESTQKQVTFNPNVNSHN 578
 QY 550 YSK-----CKSHPRAPDEPLPEQFCGSRGTLPPKRNKGTPEGLALSARDGSSAAGP 604
 DB 579 YATSRNVAEEMGAPNPMDSLAYSQ--KVSMLSRNKKAKDALGKSESA-----SHEMP 630
 QY 605 QLPGEGRSDVWQMMLESERO---SKSRHNSQSTKSTPLESARAAGEYRSHLL 661
 DB 631 VVP-EDSRNKKIQLWIEGKEKILRHKSNHSSSAKKQPELAPLSTIERGAVHPW 689
 QY 662 GASGHSRSVARHPTDPPAMPPLTPPNTLAQL-EEACRLAEVSK-----POKORCVA 715
 DB 690 VSAQLRNVPQSPHFIDPMPRPAPNPPLQLVSKRGARLEBEKKAAMPOKRL--- 746
 QY 716 SQQRDRHNSAAGAGASPANPSLAPEDHKEPKKLASVHALQASELVYTFPCGEIIPYR 775
 DB 747 -----KPOKKMVSAPQPCDNIYVAYYFCGEPIPYR 777
 QY 776 RMLKQSLTIGHEKEQOLSKKNRYEYFKKASDEFACGAVEEIMDETVPMPTEGRILK 835
 DB 778 TMVGRVYTLGQFRELTKGNRYTFKKYSDERDCGVVEEVEDMILPIYEKTIQ 837
 QY 836 VERID 840
 DB 838 VEKID 842
 RESULT 9
 AXN1_BRARE STANDARD; PRT; 835 AA.
 ID AXN1_BRARE
 AC P57094;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN 1 (AXIS INHIBITION PROTEIN 1).
 GN AXIN1.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20171051; PubMed=10704853;
 RA Shimizu T., Yamanaoka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
 RA Bae Y.-K., Hibi M., Hirano T.;
 RT *Cooperative roles of Bozozok/Pharma and Nodal-related proteins in the
 RT formation of the dorsal organizer in zebrafish.";
 RT Mech. Dev. 91:293-303(2000).
 RL CC - FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC - PFM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC - SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC - SIMILARITY: CONTAINS 1 DIX DOMAIN.
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 CC -----
 DR EMBL: AB032262; BAA92439.1; -

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DR HSP: P49799; IAGR.
DR InterPro: IPR000342; -.
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS50132; RGS; 1.
DR Developmental protein; Phosphorylation.
FT DOMAIN 92 214 RGS.
FT DOMAIN 351 436 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 437 512 BETA-CATENIN BINDING SITE (BY SIMILARITY).
FT DOMAIN 753 835 DIX.
SQ SEQUENCE 835 AA; 94351 MW; 1C62FC1F5937C87 CRC64;

Query Match 36.68; Score 1628; DB 1: Length 835;
Best Local Similarity 43.18; Pred. No. 9.2e-85;
Matches 388; Conservative 128; Mismatches 243; Indels 142; Gaps 33;

OY 7 VTLPPDSSSFREDAPRPVPGEGEPPQPS-----VGKQSTKPMVSSNARNE 59
DB 10 ICYLPDSSSTEDAPRPVPGEGEDLVSSDGRQYNSFSYSSKSDSLKNESIATPRPD 69
OY 60 DGLG-EPEGASPDSPTRMTKSLHSLGDGAYLFTFLERKCYDTLDFWFCNGFR 118
DB 70 LDGYPEGASPTPRYLKNAESLHSLDDGDIHFTFLKQEBCADMLDFWFCNGFR 129
OY 119 QMNLKD--TKLRVAKAIKYRT--ENNSVSKQLKPKATKITRIGIKQOIGSVFDDAQ 175
DB 130 KQANDENKMLAKAIKYRTILDNNGIYSRQIKPATKSEIKCVMLHIDPAMFDDAQ 189
OY 176 TEIOAVMEENAYOVLTSIDILEYVRSNGENTAVMSNG--LGSILKYCGYLTPTNEEE 233
DB 190 TEIOTMEENYPLFLKSDIYLETTRIGESPKLESDOSSVSGNKYLPGLPIYIEVE 249
OY 234 WTCADLCKLS--PTVVG-LSKTL-----RATASVSTETAEENGSRFSKSDPNVY 283
DB 250 WRQDEEQIAESDPTSPNSRLTKLLETVPQVANSKRYODNRE--YRHASWREPNVY 307
OY 284 HVGSGYFAPATSDSE--LSSDALDSDMSMTSDSVDPVPRYMSKQOLOREHRS 340
DB 308 YVNGVYLAAPATSDSQSSDA--DPLSLDSSVDGPPVRY--RKPHREIHES 362
OY 341 VKAGOVSLPFRPTNRLPKEMTVEPAPAFALISLEKLEKLESHSHSEERLOQRE 400
DB 363 AKVNGRPLPIPTNRLPKDI--HYERKFAELISLEGLVREKREKLEERLAKRRL 421
OY 401 DEEREGSE---QALSRDAP---VOHPLALPSGSY-----EEDPOTILDDHLS 444
DB 422 EEEGDADISTGPSLANHRYPAVHYGGRYSMSYNGQLRDHNEBESILDEHYQ 481
OY 445 RVLTPGCGSGVGRYSRSPDHNNHNOCHTLLSTGKLRPAACPLDGK-SF 503
DB 482 RVMTPTGCGSGTGRHSKSRSPG-----LPAGKTPG--MPLSGCGGKH 526
OY 504 LTKOTTK---HVNNH-YIHH---HAYPKTEETEAATORVRLCPG---TDYCYGS 551
DB 527 QARQPRGEAHLNHNKIHNTHTAAAGKPKQAEAEAR-----MNGGFAMNTQHNHG 581
OY 552 -KCKSH-----PKAREPLGEOFCGSRGTLPRKNAKTEPGLALSARDGMSAAG 603
DB 582 PKSRNYADGMSVGRNTMDPMG---YSSKSGTSLSKRPVKEDGNFEMRE----- 628
OY 604 POLGEEEDRQDVMOMWLESEKOS--KSKPH-SAQISIKSYPLESKRAARGEVSRNH 659
DB 629 -PLADDERKQKILQWMEGEKEGRYKSPYSGISGPKAQGHEPARSPSSVELGAVH 687
OY 660 LLGASGHSRVARAPFTQDAMPPLTPPNTLAOLEBACRLAEVSKQOKRCCVAAOOR 719
DB 688 PWYTAQLANNVQPSHFQODPTMPNPAPNPLTQLEARRLIEF----- 731
OY 720 DRNHSAGQAGAPFANPSLAPEDHKRPPKLAVALQASLAVYVTFPGCEIPIRYRMILK 779

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DB 732 ERRKSGTLQ-----AKORHKNMKK-----QPCENTVAVYFCGEPIRYTSVK 774
OY 780 AQSLLGHFKKQLSKKGYRYRYFKKASDFPACGAFVEEIMDEYLVPEGRILCKVRI 839
DB 775 GRVTLGGFKELTKRKSGYKFKVSEFGGVVEEVEDDALPLFEERIKGVKEV 834
OY 840 D 840
DB 835 D 835

RESULT 10
AXIN1_HUMAN
ID AXIN1_HUMAN STANDARD; PRT; 900 AA.
AC 015169;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN1 (AXIS INHIBITION PROTEIN 1) (AXIN) (FRAGMENT).
GN AXIN1 OR AXIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasticek T.J., Perry W.L. III,
RA Lee J.-J., Tilghman S.M., Gumbiner B.M., Costantini F.;
RT "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation.";
RL Cell 90:181-192(1997).
CC -!- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATENIN AND APC BY GSK-3B.
CC -!- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
CC TERNARY COMPLEX. MAY ALSO BINDS TO PLANOGLUBIN (GAMMA-CATENIN),
CC APC, DVL AND PP2A.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC -!- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A.
CC -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC
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DR EMBL: AF009674; AAC51624.1; -.
DR HSP: P49799; IAGR.
DR MIM: 603816; -.
DR InterPro: IPR000342; -.
DR InterPro: IPR001158; -.
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS50132; RGS; 1.
DR Developmental protein; Phosphorylation.
KM NON_TER 1 1
FT DOMAIN 1 248 RGS.
FT DOMAIN 385 470 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 471 540 BETA-CATENIN BINDING SITE (BY SIMILARITY).
FT DOMAIN 818 900 DIX.
SQ SEQUENCE 900 AA; 99803 MW; E5F990B11FC7B3B CRC64;

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Query Match 36.1%; Score 1605; DB 1; Length 900;
 Best Local Similarity 41.2%; Pred. No. 2e-83;
 Matches 382; Conservative 125; Mismatches 246; Indels 172; Gaps 29;

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QY 12 DSSSRREAPRPVPGEGETPPPCPSYGVKOSTKPMFVS-----SN 54
DB 48 DLGASTEDAPRPVAGEGE-----LVSTDPRAASVFCSCGVKIGKGNSTAT 97
QY 55 ARNRDGLG-EPEGASPSPLTMTKSLHLLGDDGATVLTFTLEBKCVDTIDFWFA 113
DB 98 PRRSDDLDCEPEGASPRPLTKAESHLSLDDDDGSLFTFLTKDGGCGLDDFWFA 157
QY 114 CNGFRQMLKDT--KTLVAKAIYKRYI-ENNSVYSKQLKPAKTYIRDGIKKOIGSV 169
DB 158 CTGFRLKEPCDSNEKKRLKLAIRKYLIDNNGVLSQTKPATSFILKCGIMKOLIPA 217
QY 170 MFDQOTELQANMENNAQVFLTSITLYEYVSGGENTAYMS--NGIGLSKVLGCVLPT 227
DB 218 MFDQOTELQATMENTYPSFLKSDIYLEYRTGSESPKVSDDSGSGSGKIGSLYPT 277
QY 228 LNEEBEWTG-----ADLKCKLSPVYVGLSKTLRAATASVRSFETAENGFRFKR 276
DB 278 LNEDEEMKCDMDDEDDRDADAPRRL-POKILLETAPRVSSSRKRSSEGRFRTGWR- 335
QY 277 SDPVAPVYGVGYAPATPSANDSE--LSSDALTDMSMTDSSVDGVPYRMGSKQL 333
DB 336 -EPVAPYVYVNGYALAPATPSANDSEQSLSSDA--DTLSLTDSSVDGIPRYRI-RKH 389
QY 334 QREMRKRVKANGOVSLPHFRPHRLPKMTVPERAFAELISRLKLEKLSHSLSE 393
DB 390 RREMQESQVAVGRPLPIPTTRTKPEVR-VEPOKFEELIHLLEAVORTREAEKLEE 448
QY 394 RLQOIREDEKESGEQALSHRDGAPVQ-----HPLALDPS-----G 429
DB 449 RLKRVMEEGE-----DGPSSGPRPCFKLPRAPAMHFRPRLCTMACAGIRD 499
QY 430 SYEDPOTIIDDHL.SRYLKTQPCGSPGVGRKSPRSRDHNNHNNQOCHTLSTGSKL 489
DB 500 AHENPESITLIDENQVRLATRGROSPG-----PGRNSPDSGHV-----AKM 540
QY 490 PRVACRLLGSKSFLTKQTKT-----HVNHHYIHHNAVPKTEELFEATORTVRC 539
DB 541 PVALGGAASGHGKHVRKSGAKLDAAGLHHNHVHHV--HHSTARPEQVDEALTRAQS 598
QY 540 LCPGCTIYCYCK-----CSHPRARPERLEBOFCGSRGGLTPRRNAKGTERTALSARD 594
DB 599 SFWAGLEPHSHGARSRGYSBSVGAAPNADGLAHSG-KVGVACRKNRAKKAESGKAST-- 655
QY 595 GGNSSAAGPOLPG--EEGRSDPVMMCMLESERO--SKSKRPSAQSTIKSYPLESARA 649
DB 656 -----EVRGASDAEKKNKIMOMITIEGEKEISRHRRTGHGSGTAKKPOPHENSRP 705
QY 650 APGERVSRHLLGASGHSRVARAHPTODPAMPRLTPNTLAOLEBACRRLAEVSK-- 706
DB 706 -----LSLEHPMAGPOLRTSVQPSHLEFIODPTMPRHAPRPLQLLEARRRLLEEERAS 760
QY 707 --PQOKOCCVASOQRDNHNSAOGASPPRANP-----SLAPEDHKPKKLASY 753
DB 761 RABSKQTYVOEVMR-----GRACVPRACAVLHVPAVSDMELSETETRSQRRVGGG 813
QY 754 HALQASELVYTFEGCEIEPYRRLKAKOSTLGFHKEQJLSKNGNYNYFYFKKADACGA 813
DB 814 SAQPCOSIYAVYFCGPRPIYKRLVNGRAVTLLOQFELLTKKSGSYRYFKVSDERDCG 873
QY 814 VFEIWDDETFLVPMYEGRLIGKVERID 840
DB 874 VFEVREDEAVLPVFEKILGKVEKYD 900
  
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RESULT 11
 AXN_DROME STANDARD; PRT; 745 AA.
 ID AXN_DROME
 AC Q9VA07; Q9XYC1;

DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN (AXIS INHIBITION PROTEIN) (DAXIN) (D-AXIN).
 GN AXN OR CG7926.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 NX NCBI_Taxid=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA MEDLINE=99174086; PubMed=10073940;
 RA Hanada F., Tomoyasu Y., Takatsu Y., Nakamura M., Nagai S.-I.,
 RA Suzuki A., Fujita F., Shibuya H., Toyoshima K., Ueno N., Akiyama T.,
 RA "Negative regulation of Wingless signaling by D-axin, a Drosophila
 RT homolog of axin."
 RL Science 283:11739-11742(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RA Ruel L., Anthopoulos N., Goncalves J., Manoukian A.S., Woodgett J.R.;
 RT "A Drosophila homolog of the axin gene is involved in the transduction
 RT of the wingless signal regulating the stability of the armadillo
 RT protein."
 RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers J.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrial J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laspo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paolel J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheibel F., Shen H.,
 RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster".
 RL Science 287:2185-2195(2000).
 [4]
 RP FUNCTION.
 RX MEDLINE=99387984; PubMed=10457025;
 RA Willert K., Logan C.Y., Atora A., Fish M., Nusse R.,
 RA "A Drosophila Axin homolog, Daxin, inhibits Wnt signaling.";

FT DOMAIN 67 184 RGS.
SQ SEQUENCE 547 AA: 59833 MW: FIBDF29E5336EF75 CRC64:

Query Match 4.4%; Score 195; DB 1; Length 547;
Best Local Similarity 23.3%; Pred. No. 0.00039;
Matches 125; Conservative 85; Mismatches 201; Indels 126; Gaps 27;

```

QY 39 SVGKQSTKPMVSSNARNEDGLGE-----PEGKASP-----DSPLTRWTKSLHSLIG 87
DB 20 SDGELTST-----AGSQOAGEGRCSSLSIHSILPSGSPSPFSTDEQPVASMAQSFERRLLQ 73
QY 88 DODGAYLFTFLERKCYVDLDFWACNGFRQMNLDKDTL-RVAAIKYKRIENNSVVS 146
DB 74 DPGGLAYFTFLERKESAEVNTFWACERFQDIPASDTKQLOAEHNIYHEFLS-----S 128
QY 147 KOLKAT--KTYIRDGIKKQOIGSVMFDOAQTEIOAVMEENAYQVFLSDIYLEYVRSG 203
DB 129 QALSPVNIIDRQAMLSEEVLAQRPD-MFRAOQQLIFNLMKFDYSARFVKSPLVQECCLAE 187
QY 204 GENTAYMNGG--IGS-----LKVLGGLPTLNEEF-----EWTCA-DLKCKLSPT 246
DB 188 AEGRLPRPGSSHLGSPDTAKKPKLPGKSLPLGVEELGOLPLAEGPCGRPLKSFRR 247
QY 247 VVG--LSSKTILR-ATASVSTETAENGFRSPFRS-DPVNRYHVGSG-----YV 290
DB 248 MTGGMNGLALRREGSGSLNSASLDGLFAYVSKSESHKSLSGSESESRPGKCV 307
QY 291 FAPATSANDELSLDALTDSSMTDS-----SVDGVPYRMS-KKOLQREMR 339
DB 308 YLPGDTA-----SLTALRPLGLTRDMLAGICEKRGSLPLDIKYVLVNEGKALVLDQC 361
QY 340 SVKNGQVSLPHFRTRHLRPEKTPVEPAFAELISRLKLELSRHSLEERLQIR 399
DB 362 TVLADQEV-----RLENKIT-----FQLELVGLERYVRISAKPTKRLQALPIL 406
QY 400 EDEKEG--SEQALSSRDG---APVOHPLALLPSGSYEEDPQTLDDHLSRVKCTPGCQ 453
DB 407 ---AKHGSLDQVVLHPRGEKQMDLETPEVSSVSAQTLVLD--TPPAKMSSEANISPRC 461
QY 454 SPVGGRYSRPSRDPHHNHHHQQCHTLSTGKRLPVVACPLLGKSKFLT--KOT 508
DB 462 SQGC---LPRQTKDHS-----LPPSSSLVEDASSSTGNROT 497

```

RESULT 13
RGS3_HUMAN
ID RGS3_HUMAN STANDARD; PRT; 544 AA.
AC 008773;
DT 01-NOV-1997 (Rel. 35, Created).
DT 01-NOV-1997 (Rel. 35, Last sequence update).
DT 01-OCT-2000 (Rel. 40, Last annotation update).
DE REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14).
GN RGS14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97312490; PubMed=9168931;
RA Snow B.E., Antonio L., Suggs S., Gutstein H.B., Siderovski D.P.;
RT "Molecular cloning and expression analysis of rat Rgs14.",
RL Biochem. Biophys. Res. Commun. 233:770-777(1997).
CC -I- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM.
CC -I- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN, LUNG, AND
CC SPLEEN. LOW EXPRESSION HAS BEEN FOUND IN HEART, LIVER, SKELETAL
CC MUSCLE AND TESTIS.
CC -I- SIMILARITY: CONTAINS 1 RGS DOMAIN.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U92279; AAC53175.1; -
DR HSP: P00778; ITAL.
DR InterPro: IPR00342; -
DR Pfam: PF00615; RGS; 1.
DR PRINTS: PR01301; RGS; PROTEIN.
DR PROSITE: PS50132; RGS; 1.
KW Signal transduction inhibitor.
FT DOMAIN 67
SQ SEQUENCE 544 AA: 59491 MW: FF6B24BD2F593B4E CRC64;

Query Match 4.3%; Score 190.5; DB 1; Length 544;
Best Local Similarity 21.9%; Pred. No. 0.00069;
Matches 117; Conservative 79; Mismatches 185; Indels 153; Gaps 24;

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QY 39 SVGKQSTKPMVSSNARNEDGLGE-----PEGKASP-----DSPLTRWTKSLHSLIG 87
DB 20 SDGELTST-----AGSQOAGEGRCSSLSIHSILPSGSPSPFSTDEQPVASMAQSFERRLLQ 73
QY 88 DODGAYLFTFLERKCYVDLDFWACNGFRQMNLDKDTL-RVAAIKYKRIENNSVVS 146
DB 74 DPGGLAYFTFLERKESAEVNTFWACERFQDIPASDTKQLOAEHNIYHEFLS-----S 128
QY 147 KOLKAT--KTYIRDGIKKQOIGSVMFDOAQTEIOAVMEENAYQVFLSDIYLEYVRSG 203
DB 129 QALSPVNIIDRQAMLSEEVLAQRPD-MFRAOQQLIFNLMKFDYSARFVKSPLVQECCLAE 187
QY 204 GENTAYMNGG--IGSLXVLGGLPTLNEEWTCDLKCKLSPT----- 245
DB 188 AEGRLPRPGSSHLGSPDTAKKPKLPGKSLPLGVEELGOLPLAEGPCGRPLKSFRR 247
QY 246 ---TVVGLSKTLR-ATASVSTETAENGFRSPFRS-DPVNRYHVGSG-----YV 290
DB 232 AEGRLPRKSFRRMPCGAVNALSRLREGSGSLNSASLDGLFAYVSKSESHKSLSGSE 291
QY 289 -----YFAPATSANDELSLDALTDSSMTDS-----SVDGVPYRMS 327
DB 292 GESESRPGKCVCCVYLPDGA-----SLTALRPLGLTRDMLAGICEKRGSLPLDIKYVL 345
QY 328 G-SKQLOREMRHSVANGQVSLPHFRTRHLRPEKTPVEPAFAELISRLKLELE 386
DB 346 GKEQKALVLDQCTVLADEV-----KLENNIT-----FQLELVGLERYVRISAK 390
QY 387 SRHSLEERLQIREDEKEG--SEQALSSRDG---APVOHPLALLPSGSYEEDPQTLDD 440
DB 391 PTKRLQALPIL---AKHGSLDQVVLHPRGEKQVLDLENVSSVSAQTLVLD--TLPD 445
QY 441 DILSRVTKPRGQSPGVGGRYSRPSRDPHHNHHHQQCHTLSTGKRLPVVAA 494
DB 446 AKTRASSIIPCRSQC---LPRQTKDHS-----LPPSSSLVEDASSSTGNROT 497

```

RESULT 14
RGS3_HUMAN
ID RGS3_HUMAN STANDARD; PRT; 519 AA.
AC P49366;
DT 01-OCT-1996 (Rel. 34, Created).
DT 01-OCT-1996 (Rel. 34, Last sequence update).
DT 01-OCT-2000 (Rel. 40, Last annotation update).
DE REGULATOR OF G-PROTEIN SIGNALING 3 (RGS3).
GN RGS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96178495; PubMed=8602223;
RA Dreyer K.M., Blumer K.J., Kang V.H., Kehrl J.H.:
RT "Inhibition of G-protein-mediated MAP kinase activation by a new
RL mammalian gene family."
RL Nature 379:742-746(1996).
CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -----
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CC -----
DR EMBL: U27655; AAC50394.1; -
DR HSSP: P49799; IAGR.
DR MIM: 602189; -
DR InterPro: IPR000342; -
DR Pfam: PF00615; RGS; 1.
DR PRINTS: PRO1301; RGS; PROTEIN.
DR PROSITE: PS50132; RGS; 1.
KM Signal transduction inhibitor.
FT DOMAIN 394 510
SQ SEQUENCE 519 AA; 56601 MW; FICFE3F27D4673A0 CRC64;

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Query Match 4.38; Score 189.5; DB 1; Length 519;
Best Local Similarity 32.08; Pred. No. 0.00074;
Matches 49; Conservative 26; Mismatches 67; Indels 11; Gaps 4;
OY 56 RRNEGGLGEPGR-----SPDS-PLTRMTKSLHSLGDODGAYLPTFLEREKCYDT 107
DB 361 RRNSPGAPRAGKADKMKKSFPTSEALKNGESLEKLLVHYGLAVQAFRTFSEEN 420
OY 108 LDFWPCNGFPGNMLKDTTLRAVAKAIYKRIENNSVSKOLKPKTYIRDCIKQOIG 167
DB 421 LEFWLACEDFEKKVK-SQSKMASAKKIFAEVIAIQACEKNLDSTREHTDNLT--QSVT 477
OY 168 SVMFDQAQTEIOAVMEENAYQVFLTSIDYLEV 200
DB 478 RGFDLAOKRIFGLMEKDSYPRFLSLDLTL 510

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RESULT 15
RGS2_HUMAN STANDARD; PRT; 211 AA.
AC P41220;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING 2 (RGS2) (G0/G1 SWITCH REGULATORY
DE PROTEIN 8).
GN RGS2 OR G0S8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA MEDLINE=94235158; PubMed=8179820;
RA Siderovski D.P., Heximer S.P., Forsdyke D.R.;
RT "A human gene encoding a putative basic helix-loop-helix
RT phosphoprotein whose mRNA increases rapidly in cycloneximide-treated
RT blood mononuclear cells."
RL DNA Cell Biol. 13:125-147(1994).
RN [2]

```

```

RP SEQUENCE FROM N.A.
RA Baguley C.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=95371353; PubMed=7643615;
RA Wu H.-K., Heng H.H., Shi X.-M., Forsdyke D.R., Tsui L.-C., Mak T.W.,
RA Minden M.D., Siderovski D.P.;
RT "Differential expression of a basic helix-loop-helix phosphoprotein
RT gene, G0S8, in acute leukemia and localization to human chromosome
RT 19p11."
RL Leukemia 9:1291-1298(1995).
CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACUTE MYELOGENOUS LEUKEMIA (AML)
CC AND IN ACUTE LYMPHOBLASTIC LEUKEMIA (ALL).
CC -1- PTM: COULD BE PHOSPHORYLATED. MIGHT BE FUNCTIONALLY REGULATED BY
CC PROTEIN KINASE(S).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L13391; AAA20680.1; -
DR EMBL: L13463; AAC37587.1; -
DR EMBL: AL035407; CAB62512.1; -
DR HSSP: P49799; IAGR.
DR MIM: 600861; -
DR InterPro: IPR000342; -
DR Pfam: PF00615; RGS; 1.
DR PRINTS: PRO1301; RGS; PROTEIN.
DR PROSITE: PS50132; RGS; 1.
KM Signal transduction inhibitor; Cell cycle; Phosphorylation.
FT DOMAIN 83 199
SQ SEQUENCE 211 AA; 24382 MW; EFPEA4E7E9AD8F CRC64;

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Query Match 3.9%; Score 172.5; DB 1; Length 211;
Best Local Similarity 26.98; Pred. No. 0.0021;
Matches 46; Conservative 24; Mismatches 72; Indels 29; Gaps 4;
OY 30 EGEPPOCPQSVGKQVS---TKMPVSSNARRNEDGLGEPGRASPDSPLTRMTKSLHSL 85
DB 50 QNSSTRPGKPKTGKSKQQAIFRSPDEAQL-----WSEAFDEL 87
OY 86 LGDDGAYLFTFLEREKCYDTLDFWPCNGFPGNMLKDTTLRAVAKAIYKRIENNSV 145
DB 88 LASKYGLAFAFALFSECEENIEFWLACEDEPKTKR-SPOKSSKARKIYDFIEKAPK 146
OY 146 SKQLPATKTYIRDCIKQOIGSVMEQDAQTEIOAVMEENAYQVFLTSIDY 196
DB 147 EINIDPOTKILIAONI--QEAISGCTTAOKRKYSLIMENNSIPRLSEFFY 195

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Search completed: October 23, 2001, 11:04:19
Job time: 142 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 23, 2001, 11:01:36 ; Search time 31.06 Seconds
(without alignments)
3578.114 Million cell updates/sec

Title: US-09-587-574-1
Perfect score: 4445
Sequence: 1 MSSAVLVTLPPSSSFRED.....DETVLPMYEGRLGKERID 840

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1295	29.1	706	13	Q9PRP2	Q9PRP2 xenopus lae
2	736	16.6	147	4	Q9H3M6	Q9H3M6 homo sapien
3	208	4.7	235	4	Q9NS28	Q9NS28 homo sapien
4	180	4.0	192	11	Q9JL23	Q9JL23 mus musculus
5	180	4.0	297	11	Q9JL22	Q9JL22 mus musculus
6	175.5	3.9	204	13	Q9I9D9	Q9I9D9 xenopus lae
7	175.5	3.9	872	5	Q9NGQ0	Q9NGQ0 drosophila
8	175.5	3.9	1175	5	Q9VCX2	Q9VCX2 drosophila
9	173.5	3.9	211	11	Q9JHX0	Q9JHX0 rattus norv
10	173.5	3.9	1510	5	Q61802	Q61802 caenorhabdi
11	172.5	3.9	829	5	Q9UB06	Q9UB06 drosophila
12	172.5	3.9	1175	5	Q9YX8	Q9YX8 drosophila
13	168.5	3.8	211	11	Q9JL24	Q9JL24 mus musculus
14	168	3.8	196	11	Q9JL25	Q9JL25 mus musculus
15	166	3.7	209	4	Q9H1M2	Q9H1M2 homo sapien
16	163.5	3.7	533	5	Q22998	Q22998 caenorhabdi
17	162.5	3.7	980	4	Q9Y3B7	Q9Y3B7 homo sapien
18	157.5	3.5	998	5	Q9W3B8	Q9W3B8 drosophila
19	156.5	3.5	1208	4	Q9HCF8	Q9HCF8 homo sapien

20	155.5	3.5	3536	5	Q9VZ30 drosophila
21	153.5	3.5	1023	11	P70588 rat mus norv
22	151	3.4	1150	3	Q99129 uscllago ma
23	151	3.4	2559	5	Q44381 drosophila
24	150.5	3.4	2472	4	Q9NS89 homo sapien
25	150	3.4	1032	11	Q9QX27 rat mus norv
26	150	3.4	2207	5	Q9U0V2 leishmania
27	149	3.4	2506	4	Q9NS88 homo sapien
28	149	3.4	2559	5	Q44113 drosophila
29	148.5	3.3	413	5	Q9N817 trypanosoma
30	148.5	3.3	1380	5	Q77086 drosophila
31	148.5	3.3	2417	5	Q9VAS9 arabidopsis
32	148	3.3	684	10	Q9SG87 arbidopsis
33	148	3.3	1783	4	Q15038 homo sapien
34	148	3.3	1791	4	Q60382 homo sapien
35	148	3.3	2296	4	Q9UHA8 homo sapien
36	148	3.3	2559	5	Q9V7X3 drosophila
37	148	3.3	3851	4	Q43161 homo sapien
38	148	3.3	3926	4	Q9UPA5 homo sapien
39	147	3.3	1200	5	Q25388 loligo peal
40	146	3.3	2752	4	Q9UQ35 homo sapien
41	145.5	3.3	1436	5	Q9VH03 drosophila
42	145	3.3	2237	5	Q9V122 drosophila
43	144.5	3.3	997	4	Q9Y4G1 homo sapien
44	144.5	3.3	1019	4	Q9Y4G7 homo sapien
45	144.5	3.3	1162	5	Q9VWB7 drosophila

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	706 AA.
ID	Q9PRP2			
AC	Q9PRP2			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	AXIN-RELATED PROTEIN.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_Taxid=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=OVARY;			
RA	Itch K., Antipova A., Ratcliffe M., Sokol S.;			
RT	"Dishevelled transduces a signal by displacing GSK3 from axin-GSK3 complex".			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF140243; AAF22574.1; -.			
DR	InterPro; IPR000342; -.			
DR	InterPro; IPR001158; -.			
DR	Pfam; PF00778; DIX; 1.			
DR	PRINTS; PR01301; RGSPROTEIN.			
DR	SMART; SM00021; DAX; 1.			
SO	SEQUENCE 706 AA; 79196 MW; C3D0AF0D9540F162 CRC64;			
Query Match	29.1%; Score 1295; DB 13; Length 706;			
Best Local Similarity	38.5%; Pred. No. 4.1e-86;			
Matches 327; Conservative 114; Mismatches 251; Indels 158; Gaps 24;				
OY	1 MSSAVLVTLPPSSSFREDAPRPVPEEGETPPCPQSVGVKQSTKMPV---SSNARR 57			
DB	1 MSSAGVLCIPDSGPIFRETSLRPVPCOE-----TNFKPEKFTMDSOHLKH 48			
OY	58 NDDGGEPEGRASPSPLTRKTKLSHSLGDDGAYLRTFLERKCYDITDFWACNGF 117			
DB	49 KEDFNREAGCVAHDSRSRWGRSLNLLDDODGATFLFRMYLEGGLDILLTFWACNGF 108			
OY	118 ROMNLKDKTKTLVAKAIYKRYIENNSVSKLKPATYTYIRDIKKQOIGSVMPDOAQTE 177			

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Db 109 RAADPLEPTSKAKAIYMYONSSAVSGRLKPTTRTQVKECVKHNQJNKTVPDQAOE 168
Qy 178 IQAVMEENAYOVFLTSDIYLEYRGSGENTATMSNGSLGSLAVGLYPTLMEBEWICA 237
Db 169 IQRAMOEAFSTLSQSDICEYAR-GVEDSPPEPSGP-LEPTLEDEFG- 217
Qy 238 DLKCLSPITVGL-----SKTLRATASVSTETAEENFRSFRKSDPVPNPHVSGVYF 291
Db 218 -----GLHFRSGMGKINRAFSRI-----PPRNRSHFRLEQYQY-----F 255
Qy 292 APATSANDELSDALITDMSMTSSVYGVPRYMGSKQLOREMHSVKANGVSLPH 351
Db 256 APRASTINDEISSDALTEDMSMTDGVGIPYR--SKK--QREIHRSVANGKYSIPF 311
Qy 352 PPRTRHLEKMTVPBPAFAELISLEKLELESRLSELELOIREDEKESDAL 411
Db 312 VRTYRPRAEKMTSPRAEAAKLTALLEVKKORAEKEKLORELEIADYDIPS 371
Qy 412 SSGDAPVOHPLALLPSGSEEDPQTILDLHSLVLTGPGOSPGVGYSPRSRSPDHH 471
Db 372 SSHE-----TVPGALEDPOSLDDHVSRLKTP-----ANLSPRSOSP----- 411
Qy 472 QHNNHQCHTLTSTGKILPRVACPLLGSKFLTKOTKHYNNHYNHNAVPKTEIEA 531
Db 412 -----FYQKRGKFP-----AFSKQTSLSCHLR-----PKVPOGMEA 444
Qy 532 EATORVRLCIPGTDYUVCYKSKSHPKAREPLRPGFCGSGTGLPKRNAKTEPGALS 591
Db 445 TST-----LASELRSSVSQOLRRSRK---PGGCTOPHREEGTANAVLT 487
Qy 552 ARDGMSSAAGPOLPGEGRSDOVQWMLSESRQSKSPHSAOSIRKSYPLESANAP 651
Db 488 -----PLSPDEAEARNHSLQWVLDSAK-----LMKKHRETAIVTP 524
Qy 652 GERVRHNLGASGRSVARAHPTODRAMPRLPTTLAQLAEACRLAE---VSKPO 708
Db 525 CPELKK-----ATHRAASOPAHPLFLODTSMPLTAPRTLDQLEARRRLVEDKRPKLH 578
Qy 709 KORCCVASOORDRNHSAAGAGAPFANPSLAPDHKEPKKLASVHALQASELVVTFYC 768
Db 579 KSRCSVSTTLKEKGTAE-SVSSSGFTLKLS-BEQKTAKPPSS--BCPOGLAIIVYFC 634
Qy 769 GEELPYRMLKAOSLTGHEFQOLSKGNRYTKKASDEPACAVAEETIMDETIVPMY 828
Db 635 GERIPYIRTEPSTLQEFKELLKSGSNKYYPKKESHFEPCNAVQVESEDAVLPLF 694
Qy 829 EGRTIGYVER 838
Db 695 EKITICKVER 704

RESULT 2
Q9H3M6 PRELIMINARY; PRT; 147 AA.
AC Q9H3M6;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
GN CONDUCTIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakamura Y., Furukawa Y., Takahashi M.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Takahashi M., Furukawa Y.;
RT Identification of 3' UTR of Axin2."

```

```

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB052751; BAB19762.1;
FT NON_TER 1
SQ SEQUENCE 147 AA; 16771 MW; 324562918E7A577A CRC64;

Query Match
Best Local Similarity 94.6%; Score 736; DB 4; Length 147;
Matches 139; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 694 LEACRRLAEVSKPKQKRCVSAOQRDRNHSAGAPFANPSLAPEDHKEPKKLASY 753
Db 1 LEACRRLAEVSKPKQKRCVSAOQRDRNHSATYQTATFPSPSLAPEDHKEPKKLAV 60
Qy 754 HALDASELVVTFYFCGEIEIPYRMLKAOSLTGHEFQOLSKGNRYRYFKKASDEFACGA 813
Db 61 HALDASELVVTFYFCGEIEIPYRMLKAOSLTGHEFQOLSKGNRYRYFKKASDEFACGA 120
Qy 814 VFEETIMDETIVPMYEGRTIGYVERID 840
Db 121 VFEETIMDETIVPMYEGRTIGYVERID 147

RESULT 3
Q9NS28 PRELIMINARY; PRT; 235 AA.
AC Q9NS28;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING 13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Yuan Z., He L., Cao X.;
RT "A novel regulator of G-protein signaling."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076642; AAF80227.1;
DR InterPro; IPR000342;
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PRO1301; RGSBPROTEIN.
SQ SEQUENCE 235 AA; 27582 MW; 973ABDE8EC7DE3D5 CRC64;

Query Match
Best Local Similarity 4.7%; Score 208; DB 4; Length 235;
Matches 56; Conservative 34; Mismatches 58; Indels 34; Gaps 6;

Qy 41 GKVOSTKPMVPVSSNMARN-----ED-----GLGPEGRASPDSPLTWTSTSL 82
Db 29 GKETKKEAKIKAKERKNRLSLVQKPEFHEDTSSRSGHLAKETRVPEEAV-KWGSF 87
Qy 83 HSLLDGQDGAFLFRFLERKCVDTLDWFACNGFR-----QNNLKQTKTLRVAKATYK 136
Db 88 DKLLSHRDGLEAFRFLKTFESEENIEFWIACEDPKKSGPOHILK-----AKATYE 140
Qy 137 RYIENNSVYSKQLKATYTIIDGIRKQOIGSVMPDQATELQAVMEENAYOVFLTSDIY 196
Db 141 KFIQYDAPKEVNLDPHTKEVTINSTITOPTLHS--FDAOSRYQLOMEDSYTRFLKSDIY 198
Qy 197 LE 198
Db 199 LD 200

RESULT 4
Q9JL23 PRELIMINARY; PRT; 192 AA.
AC Q9JL23;
DT 01-OCT-2000 (Tremblrel. 15, Created)

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DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
 DE REGULATOR OF G-PROTEIN SIGNALING 3S.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/C; TISSUE=KIDNEY;
 RX MEDLINE=20243574; PubMed=10779778;
 RA Relf K., Cyster J.G.;
 RT *RGS molecule expression in murine B lymphocytes and ability to down-
 regulate chemotaxis to lymphoid chemokines.*;
 RL J. Immunol. 164:4720-4729(2000).
 DR EMBL: AF215669; AAF34626.1; --
 DR InterPro: IPR000342; --
 DR Pfam: PF00615; RGS; 1.
 DR PRINTS: PR01301; RGS-PROTEIN.
 DR ProDom: PD001580; --; 1.
 SQ SEQUENCE 192 AA; 22501 MW; BE6E0C1FE07952F CRC64;

Query Match 4.0%; Score 180; DB 11; Length 192;
 Best Local Similarity 28.2%; Pred. No. 1.4e-05;
 Matches 48; Conservative 31; Mismatches 67; Indels 24; Gaps 4;

OY 32 ETRPCOPSYGVKQSTKPM-PVSSNARNEDGLGEPGRASPDSPLTRMTKSLSLGDDOD 90
 DB 37 ESRGAPASKTKTKTSFPTSEEA-----LKWSESLKLLHRY 76
 OY 91 GAYLFFPTLERKCVDTLDFWFCNGFRONMLKDTLVAKAIRYIENNSVSKOLK 150
 DB 77 GLEVFQAFRTFSESENLDFWLACEDFKYK-SQSKMAKAKKIFAEFIAIQACKEVNLD 135
 OY 151 PATKTYIRDGIRKQOIGSVFDOAQTEIQAVMEENAYQVFLTSIDILEYV 200
 DB 136 SYTREHTKENL--QSITRCGFDLAQRIRFGLMKDSYPRFLRSLDYLDI 183

RESULT 5
 OY 09JUL22 PRELIMINARY; PRT; 297 AA.
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
 DE REGULATOR OF G-PROTEIN SIGNALING 3 (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=20243574; PubMed=10779778;
 RA Relf K., Cyster J.G.;
 RT *RGS molecule expression in murine B lymphocytes and ability to down-
 regulate chemotaxis to lymphoid chemokines.*;
 RL J. Immunol. 164:4720-4729(2000).
 DR EMBL: AF215670; AAF34627.1; --
 DR InterPro: IPR000342; --
 DR Pfam: PF00615; RGS; 1.
 DR PRINTS: PR01301; RGS-PROTEIN.
 DR ProDom: PD001580; --; 1.
 FT NON_TER 1
 SQ SEQUENCE 297 AA; 33683 MW; ADF80985150B525C CRC64;

Query Match 4.0%; Score 180; DB 11; Length 297;
 Best Local Similarity 28.2%; Pred. No. 2.5e-05;
 Matches 48; Conservative 31; Mismatches 67; Indels 24; Gaps 4;

OY 32 ETRPCOPSYGVKQSTKPM-PVSSNARNEDGLGEPGRASPDSPLTRMTKSLSLGDDOD 90
 DB 142 ESRGAPASKTKTKTSFPTSEEA-----LKWSESLKLLHRY 181
 OY 91 GAYLFFPTLERKCVDTLDFWFCNGFRONMLKDTLVAKAIRYIENNSVSKOLK 150
 DB 182 GLEVFQAFRTFSESENLDFWLACEDFKYK-SQSKMAKAKKIFAEFIAIQACKEVNLD 240
 OY 151 PATKTYIRDGIRKQOIGSVFDOAQTEIQAVMEENAYQVFLTSIDILEYV 200
 DB 241 SYTREHTKENL--QSITRCGFDLAQRIRFGLMKDSYPRFLRSLDYLDI 288

RESULT 6
 OY 09JUL22 PRELIMINARY; PRT; 204 AA.
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
 DE RGS4 PROTEIN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OX NCBI_Taxid=83355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu C., Zeng Q., Blumer K.J., Muslin A.J.;
 RT *RGS Protein Inhibits Xwnt-8 Signaling in Xenopus Embryonic
 Development.*;
 RL Submitted (May-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF263451; AAF70201.1; --
 DR InterPro: IPR000342; --
 DR Pfam: PF00615; RGS; 1.
 DR PRINTS: PR01301; RGS-PROTEIN.
 SQ SEQUENCE 204 AA; 23167 MW; 31D80DAE6C38120A CRC64;

Query Match 3.9%; Score 175.5; DB 13; Length 204;
 Best Local Similarity 27.6%; Pred. No. 3.2e-05;
 Matches 42; Conservative 37; Mismatches 68; Indels 5; Gaps 3;

OY 61 GLGEPGRASPDSPLTRMTKSLSLGDDGAYLFFPTLERKCVDTLDFWFCNGFRON 120
 DB 41 GYKPPSQYVRQDEVKMAESLENLNNECGLAARFSLQSEIENIDFWACENYKKI 100
 OY 121 NKDTLVAKAIRYIENNSVSKOLKPATKTYIRDGIRKQOIGSVFDOAQTEIQ 180
 DB 101 KTG-ARLPQAOQIYEDFISVATKEVNDLSVTRFETSNILQPTVST--FDEAQHKIFI 157
 OY 181 VMEENAYQVFLTSIDILEYV--SGGENTAYM 210
 DB 158 LMEKDSYRRFLKSKFYLDIVNLSSGASTYK 189

RESULT 7
 OY 09JUL22 PRELIMINARY; PRT; 872 AA.
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
 DE REGULATOR OF G-PROTEIN SIGNALING LOC0 III.
 GN LOC0 OR CG5248.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paulirana S.V., Zhao D., Bownes M.;

"Loco III a new transcript of the RGS gene loco."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF245455; AAF62552.1;
 DR Flybase: FBgn020278; loco.
 DR InterPro: IPR000342;
 DR InterPro: IPR003109;
 DR InterPro: IPR003116;
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF02196; RBD; 1.
 DR PRINTS: PRO1301; RGS-PROTEIN.
 DR SMART: SM00390; GLOCO; 1.
 DR SMART: 872 AA; 96116 MW; 65386560A9PB40 CRC64;

Query Match 3.9%; Score 175.5; DB 5; Length 872;
 Best Local Similarity 19.4%; Pred. No. 0.0023;
 Matches 166; Conservative 138; Mismatches 355; Indels 193; Gaps 36;

DB 123 VPKVLTTPAPSAITASVAAGCAQDHG--CPSS---WAGSFEMLDAAAGMOTFEPL 176
 QY 100 EEKCVDTLDFWFCNGFRQNLKDTKLTVAKA--IKRYTENNVS---VSKLKPAT 153
 177 KKEFAENITFTACERR--LLESEADRYAQAAREIFAKHLANNSSDPVNVDSOARSLT 233
 DB 154 KTYIRDGIRKQOIGSVEMDQATEIQAWEENAVQVLTSLDYLEIVRSGGENTAYMNG 213
 234 EEKLDAAPD-----IFAPAQKQIFSLMKFDSYGRFIRSDLYKSCVEAEKQNGLPYSG 287
 QY 214 -GLSLKVLGCLPTLNEEEMTCADLCKSLPTVYVGLSSKTLKATVASTETENGFR 272
 288 LDLDLLELTNFIHLGAFSKIKK--SASNAEDRRKSLPMHMKRT--RSKSRDTEIADQMH 344
 QY 273 SFKRSDPNYPYVSGYAFAPATSAN-----DSELSDALTDMSMTDSSVDGPYR 326
 345 ALMPRPV-PQN-----APLTSASLKYCGQNSLDLHSRSSLSFDA---GTATGG 393
 QY 327 MGSKQQLQREMHRSYKANGVSLPHFPTHTLLPKEMTEVERPAFAELLISLEKLELE 386
 394 OGASTESYVSLCRVILTDGATTI-----VOTRGETVGEIYERL-----LE 434
 DB 387 SRHSLEERLQRIREDEKEGSSQALSSRDGAPVQPHALLRSGSTEEDPOTILDDHLSRV 446
 435 KRN-----LVYRYDVFQSGTKSID-----VOOPQSLG-----KEVYIERVAFK 477
 QY 447 LKTPCQSPGVGRYSRSPRSDHNNH-----HHNHOCCHTL----- 483
 478 LDLP--DPKV--ISVSKRPKKQLHEVIRPLISKNYNMEQOYIMRTQYRIDLNQVPT 532
 QY 484 -----STGKLRPVVACPLLGKSFLLTKQTKVHHHHYIHHHNAVPT 525
 533 MADGQRLIVWNSDFOYGGSSMPKOSKPMKRLPOGHLELTAKVNEELASKA----- 588
 QY 526 KEETEAETQVRCCLPCPGTDYCYCKSKSHPKAPEPLPGPOFGSRG-----TLPKR 579
 589 -----DAAASEKRPV-----DLCSMKSNKAPSETSSLFEMRRQQRGGINIPASKPLKL 638
 QY 580 NAKTEPGLIASRDGSSAAGPOLP-----GEGDRSQDVMQWMLSESRSSKSPISA 635
 639 KKKTSV--SQOSEEAATQVADPKKPIIAKLKAGVQLQ-----VTEVAHEHQDILL 689
 QY 636 QSIKSY--PLESARAA-----PEGRYSRIHLLGASHSSV--ARAHPTQDPAPEPLT 686
 690 EGLRRAQLARLEDQRTINFDLDFLKNKENSAAVSKLRKVNASLSPEVSKVATP--- 746
 DB 687 PPNTLAOLEEACRLAEVSKPOKORCCVAAQOQRBNSHSAQAQAGSPAN--PSLAPBDH 744
 747 -----TELPQAPRLSITRSQQVSPKVVDOEPETDLPAAQ--DQTEAKAPPLPPKPK 800
 QY 745 KEPKRLASVHALQASSELVVTFFCGEELPYRRM-----LKAQSLHGFHKEDLS 793
 DB 801 VLPKPSMWGVAQD-----TGNYNKYSPSKQVTPSPKEAKPGTFASKITLDLGRKSL 855

QY 794 KKGNYRYFKKASDEF 809
 DB 856 EAGSRCAVLDEPSSSF 871
 RESULT 8
 ID 09VCX2 PRELIMINARY; PRT: 1175 AA.
 AC 09VCX2.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE LOCO PROTEIN.
 GN LOCO OR CG5248.
 OS Drosophila melanogaster (Fruit fly).
 OC Euarystola; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celhiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Bokoyva D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ideyem C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen T.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003739; AAF56033.1;
 DR HSSP: P49799; IAGR.
 DR FLYbase: FBgn020278; loco.
 DR InterPro: IPR000342;
 DR InterPro: IPR003116;
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF02196; RBD; 1.
 DR PRINTS: PRO1301; RGS-PROTEIN.
 DR SMART: SM00315; RGS; 1.
 SO SEQUENCE 1175 AA; 129703 MW; 0B9811610122AC59 CRC64;

Query Match 3.9%; Score 175.5; DB 5; Length 1175;
 Best Local Similarity 19.4%; Pred. No. 0.00034;
 Matches 166; Conservative 138; Mismatches 35; Indels 193; Gaps 36;

40 VGVOSTKPMVSSNARNEDGLCEPGRASPDSPLTRMTKSLHSLGDDGAYLFRFTL 99
 426 VPKVLTTPAPPSATIASVAEAGADHG--CPSS---WAGFEMLDADAGMFFSEFL 479
 100 EREKCVDTLDWFACNGRGMNLAKDTKLRAKA--YKRYIENNSV---VSKOLKPMY 153
 480 KKEFSAENIYFTACERYR--LLESEADRYAQAREIFAHLANNSSPPVNVDSQARSIT 536
 154 KTYINDGIKKQIGSVMFDOAQTEIOAVMEENAVOVFLTSDIYLYVSGGENTAYMSG 213
 537 EKLDAAPD-----ITAPAKOKIPLSLKPFDSYORFTRSDLYKSCVEAEQNOPLPSG 590
 214 -GLGLKVLGCVLPTLNEEENTCADLCKSLPTVVGSLSKTLRATASVSTETAENGR 272
 591 LDLDLKLTKNHLGAFSKLK--SASNAEDRRKSLPMMRK--RSKSDRTEIMADQH 647
 273 SFKSDPVPNPHVSGYFAPATSAN-----DSELSDALTDDSMKTDSSVDGVPYR 326
 648 ALMPAPV-PON-----APLTASLKLVCQNSLSDLHSSRSSLSFPA---STATCG 696
 327 MGSKQOLREMHRSVKANGQVSLPHFPRTHRLPKEMTPVPAFAAELISRLKLELE 386
 697 OGASTESVSLCRVILTDATTI-----VOTRPEYVGLERL-----LE 737
 387 SNHSLERLOQIREDEKESEALSRDGAQVPHLALPGSYEEDPOTLIDHLNRV 446
 738 KRN-----LVRYVDIVFGSTKSID-----VQOPSOILAG-----KEVIERVAK 780
 447 LKTPCCSPGCGVGRSPRSRPHNQ-----HHHQOCHTL----- 483
 781 LDLP--DPKV--ISVKSPPKQOLHEVIRPLSKYNYKMEQOVIMRDTQVPIDLNQPV 835
 484 -----STGKLRPVACRPLLGKSPFLTKOTTKNHNHNNHNAVPKT 525
 836 MADGRLRIWVNSDFOVGGSSMPKOSKPKRPLQCHLDELTKNFELIASKA---- 891
 536 KEIEAEATQRYRCLPGCTDYCYCSKSHPKAREPLRGEOFGSCRG-----TLPRK 579
 892 ----DAASEKRPV-----DLCMSKSNEARSETSSLEFRNRRODRCGNIPASKPLRL 941
 560 NAKTEPLAISARDGSSAAGPOLP---GEEGRSDQVWQMLESEROSKSKPMSA 635
 942 KKKSTSS--SQOSEEAATQAVADPKPIIAKLKAGVKLQ-----VTERVAHQDELL 992
 636 OSIRKSY--PLESARAA-----PGEVSRHLLLGASGHSRV-ARAHFTODDPAMPRL 686
 993 ECLKRAQLARLEDQTEINFDPRLKKNELSAVSKLRVRSLSVSKVPTP--- 1049
 687 PPNLTALQLEACRLAEVSKPOKRCVCAVQORDRNHSAAGASPFAN--PSLAPEDH 744
 1050 -----TEIPQAPRLSTIRSQOVPSPMKVDORPETDLRAITQ--DOTEFAKAPRPLPKK 1103
 745 KEPKLASVHALQASSELVVTFFGCEELPYRM-----LKAOSLTLGHRKQOLS 793
 1104 VLPKPSWNGVAPQ-----TGNYCNKSPSKQVPTSPKASKPGTFAKRIPLDLRKSLDE 1158
 794 KKNGRYTFKKASDEF 809
 1159 EAGSRCAIYDEPSSSF 1174

RESULT 9
 Q9JHXO PRELIMINARY: PRT: 211 AA.
 AC Q9JHXO: 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE REGULATOR OF G-PROTEIN SIGNALING PROTEIN 2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE DAWLEY; TISSUE=THORACIC AORTA SMOOTH MUSCLE;
 RA Grant S.L., Lassegue B., Giendling K.K.,
 RI "RGS2 regulates angiotensin II signaling in vascular smooth muscle.";
 RL Submitted (Jun-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF279918; AAF85981.1; -
 DR InterPro; IPR000342; -
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGS-PROTEIN.
 SQ SEQUENCE 211 AA; 24323 MW; 84B5525CB41EA964 CRC64;

Query Match 3.9%; Score 173.5; DB 11; Length 211;
 Best Local Similarity 29.2%; Pred. No. 4.7e-05;
 Matches 50; Conservative 23; Mismatches 65; Indels 29; Gaps 6;

30 EGEPPOCPVSK--VOST--KMPVSSNARNEDGLCEPGRASPDSPLTRMTKSLHSL 85
 50 QNSTPGKPKTKGSKQCFIKRSP-----EAL-----LMADAFDEL 87
 86 LGDDGAYLFRFTLEKRCVDTLDWFACNGRGMNLAKDTKLRAKAIYKRYIENNSV 145
 88 LASKYGLAFAFLSEFCEENIEFWMACEDEPKRK--SPQKSSKARKLYTFOFIEKAPK 146
 146 SKOLPARKTYIRDGIRKKQIGSVMFDOAQTEIOAVMEENAVOVFLTSDIY 196
 147 EINIDPQTKTILAIQNI--QEAISGCTTAQKRYVSLMENSIPRLESSEFY 195

RESULT 10
 061802
 ID 061802 PRELIMINARY: PRT: 1510 AA.
 AC 061802:
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE H1LE01.3 PROTEIN.
 GN H1LE01.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copest T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., Mcmurtry A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smailton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RT Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Geisel C., Wamsley P.,
 RL Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;

RA Waterston R.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF067222; AAC17017.1;
 SQ SEQUENCE 1510 AA; 166889 MW; C1C08ACBC6D6FF11 CRC64;

Query Match 3.9%; Score 173.5; DB 5; Length 1510;
 Best Local Similarity 18.1%; Pred. No. 0.00068;
 Matches 168; Conservative 122; Mismatches 339; Indels 299; Gaps 40;

QY 13 PSSFFEDAPRPVPCGEETPCPSVGVKYSTKMPVSSN-----ARRNEDGIG 63
 DB 255 PTTTRRKDS-----NRLRPINPHKRVVPTKPPAPVLOQITRLPPAKKPPASRG 306
 QY 64 EEEGRASDPILTRWTKSLHSLGDGAYLRLTLEEREKCVDTLDFWACNGFQMLK 123
 DB 307 RPSNKRQTTTTTTTTTSVS-----KSPQIS 332
 QY 124 DTKTL-----RAKATIKYIENNSVSKOLKPA-----TKTY 156
 DB 333 DNTLPTLPSTVTRGIFGAAAAATAAIGTAIIMDTLIDEPSPRPRIPLVETQKTF 392
 QY 157 IR---DGIR-KQOIGSVFDOATEIOAVM---ENAYVFLSDYL-----EYV 200
 DB 393 DRTSPTDGVQVDEVPPELIDKLADSEDEVEKLAEOEIOEFIPKOVLDNADPSHGDE 452
 QY 201 RSGGENTAYMNSGGLGSLKVLGYPPLTNEEEMTCA-----DLCKLSPTVVGSLSKTL 255
 DB 453 DSDSP-----PEYAEEDREPLAVOVOLHEQVDS----- 482
 QY 256 RATASVSTETAENGFRSFKRSDPVNRPVHSGVYFAPATANSLSLSD-----ALTDSD 311
 DB 483 -PTSNVTDOSPRE---MYQHSER-----SPALSPDASVESEHERPARSPPT 526
 QY 312 MSMTDSVVDGVV--PYMGSKKQOLREMHRSYKANGVSLPHFPTNRLPREMTPEVEPA 369
 DB 527 LVTFEOSTEDAPESPEVNEVHHVQTEAQOSPVIVHSTHVEHFD--TH---DESPQSVL 581
 QY 370 FAEELISLEKIKLELRHLEERLOIRD-----PEKESGECALSSRGAPVQH 421
 DB 582 -----SVHGEGEREDHDEAPVLSVHTDHKAHSEVDPSS---PVOS 620
 QY 422 PLALLPSGSEVEDPQ---TILDDHLSRYLTKPCGQSPGVG--RYSPPRSRSP-----DH 469
 DB 621 VHSSHASEHIDEAPQPVSPVSHSHASHIEQELPLSPVASERVPVSAESPLVQSENFH 680
 QY 470 HHQ-HHHH-----QQCHTLISGCKLPPVAAACPLLGKSFGLKQTTKHVHH 515
 DB 681 HAEVHSHASEHIDEALPSPVQSVHSHDHDRSSPVASEPARSPVQSGRTSEHFEHR 740
 QY 516 -----YIHHNAVPTKEIEAEATQRYVRCLOPGTDVYCYKCKSH----- 556
 DB 741 GEVQSPSSNQFHSSEHIEERKQSPVTNQESVHSPHASEHFEHREVVPHSPASQEEFGR 800
 QY 557 -PKAREPLRGEOF---CGSRGGLPKRNKAGTEBGLALS-----ARDGMS-- 599
 DB 801 SPVSHPSVSEHFEHNEAQSPPVASQEEAARSPSVHSHASEHFEHNEHRODSPPVASE 860
 QY 600 -AAGGPOL---PGEEDROSDVQMMLESEERQSKRPHSAOSTIRKYPLESAARABGER 654
 DB 861 KAASPSVHSHASEHSEHROEIQHSPPASQNEAARSP--SVHSHASEHIEH---HGES 915
 QY 655 V-----SRHLLGASGH-----SRSYARAHFPGQ-----DP 680
 DB 916 LQSPVASMSEHNNMAESSEYTTSEKEISPIFSSTHSQDFEQOQSNFVASERDNRSR 975
 QY 681 AMPPLRPNTLAOLEACRRLAEVSK--POKORC-CVAQO-----QRDRHNSAAGQAS 732
 DB 976 TFESSVTMAAARPLSPAASHAQAARSPSEFERAPSLHQLSLNLEHDDNSAVVEAGOE 1035
 QY 733 PFANPSLAPEDHKEPKLAVYHALQASE 760
 DB 1036 PATQSPITPLEQEGRFERRAASVNSYQASE 1063

RESULT 11
 Q90B06 PRELIMINARY; PRT; 829 AA.
 AC Q90B06;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE REGULATOR OF G-PROTEIN SIGNALING LOCO C1.
 GN LOCO OR CG5248.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99180581; PubMed=10079238;
 RA Granderath S., Stollwerk A., Greig S., Goodman C.S., O'Kane C.J.,
 RA Klammt C.;
 RT "Loco encodes an RGS protein required for Drosophila glial
 RT differentiation."
 RL Development 126:1781-1791(1999).
 DR EMBL: AF130745; AAD24581.1; -;
 DR HSSP: P49799; IAGR.
 DR FLYBase: FBgn0020278; Loco.
 DR Interpro: IPR003142; -;
 DR Interpro: IPR003116; -;
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF02196; RBD; 1.
 DR PRINTS: PR01301; RGS-PROTEIN.
 DR ProDom: PD001580; -; 1.
 DR SMART: SM00315; RGS; 1.
 SQ SEQUENCE 829 AA; 91446 MW; 5C979C2F11B8FEFF CRC64;

Query Match 3.9%; Score 172.5; DB 5; Length 829;
 Best Local Similarity 19.1%; Pred. No. 0.00036;
 Matches 166; Conservative 136; Mismatches 349; Indels 217; Gaps 36;

QY 40 VGVQSTKRPVPSNARNEDGIGEPGRASPDSPILTRWTKSLHSLGDGAYLFRTEL 99
 DB 80 VPKVLTTPAPPSALTASVAEGAQDHG--CPSS---WAGSFERMLDPAAGQTFSEPL 133
 QY 100 EREKCYDTLDFWACNGEFGOMNLKDTFLPVAKA--YKRYIENNSV---VSKOLKPT 153
 DB 134 KKEESAENIYFWACERYR---LLESEADRYAQAAREIPAKHLANNSSDPVNDQARSIL 190
 QY 154 KTYIRDCIKKQOIGSVFDOATEIOAVMEENAYOVFLTSDIYLEVYRSGGENTAYMSG 213
 DB 191 EEKLADAAPD-----IFAPAKOIFSLMKFDYQRFIRSDLYKSCVEAEQKNQPLPYSG 244
 QY 214 -GLGSLKVLGCVPLTNEEEMTCA DLKCKLSPTVVGSLSKTLRATASRSTETAENG 272
 DB 245 LDDELKLTNFHIGATSKLTK--SASNAEDRRKRSLLPMHRT--RSKSDRTEIMADMOH 301
 QY 273 SFKRSPPVNPYHVGSGYVAPATSAN-----DSELSDALTDSDSMDSVSDGVPPYR 326
 DB 302 ALMPAPPV-PQN-----APLTSASLKLVCQNSLSDHSSRSSLSFDA---GTATGG 350
 QY 327 MGSKQLOEMHRSYKANGVSLPHFPTNRLPREMTPEPAFAELISLEKIKLELE 386
 DB 351 OGASTESVSLGRVILITLDATYI-----VQTRPGETVGEIVERL-----LE 391
 QY 387 SRHLEERLOIRDEERKESQALSSRGAPVQHPALLPBGSTEEEDPQITLDHLSRV 446
 DB 392 KRN-----LVTPYDVLVFGSTKSID-----VQPSQTLAG-----KEVIERVAVK 434
 QY 447 LTPGQSPGVGRYSRSPRSDPHHQ-----HHHQCHTL----- 483
 DB 435 LDLP---DPKV---ISVKSFRKKQHLHEVIRPLISKYINKEQVQVIMRDTQVPIDLNOPT 489

OY 484 -----STGKLRPVACRLGKSEFLTKOTTKHVHHYIHHNAVPT 525
DB 490 MADGRLRIYVNSDFVGGSSMPKQSKPKRLPGCHLDELTKVFNELLASKA----- 545
OY 526 KEELIATATORVRLCLPGCTDYCYCSKSHPKAPRLPGEOFGSROGTLPRKNAKTE 585
DB 546 -----DAAASE-----KSRP-----VLCMSKSNAPSESSLFE 575
OY 586 PGLALSARDGSMSSAAGPOL-----PGEGRSDQDVMQ-----WMLE 623
DB 576 -RMROORDGDNIPASKLPKLKKSTSSQOSEEAATGTAVDPKPKLIAKLKAGVKLOV 634
OY 624 SEROSKSPHSAOSIRKSY--PLESARA-----PGEVRNHLGLGASHRSV-ARAH 674
DB 635 TERVAEHOEDELLEGLKRAQLARLEDQRTETINFDLPRLKKNENISAUVSKLRKVASLS 694
OY 675 PFTODPAMPRLTPNTLAOLEBACRLAEVSKPQORCCVASQQRDRHNSAAGASPF 734
DB 695 PVSIVPATP-----TEIQPAPRLSITRSQOPVSPMKVDOEBETDLPAATQ-DQTEF 745
OY 735 AN--PSLAPEDHKEPKLASVHALQASLVVTFPCGEEIYRRM-----LKAQ 781
DB 746 AKAPRPLPPKPKVLPKPSNMGVAOP-----TGNYCNKYSPOKVPSPKESKPTGTFAS 800
OY 782 SLTLGHFEOLSKKGNRYEYFKKASDEF 809
DB 801 KIPLDLGRKSLLEAGSCAVILDEPSSSF 828

RESULT 12
O9XYX8 PRELIMINARY; PRT; 1175 AA.
AC O9XYX8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING LOCO C2.
GN LOCO OR CG5248.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OY NCBI_TaxID=7227;
R [1]
I SEQUENCE FROM N.A.
RX MEDLINE=99180581; Pubmed=10079238;
RA Grandenath S., Stollewerk A., Greig S., Goodman C.S., O'Kane C.J.,
RA Klemm C.;
RT "Loco encodes an RGS protein required for Drosophila glial
RT differentiation."
RL Development 126:1781-1791(1999).
DR EMBL: AF130744; AAD24580.1; .
DR HSSP: P49799; IAGR.
DR FLYBase: FBgn0020278; loco.
DR InterPro: IPR00342; .
DR InterPro: IPR003109; .
DR InterPro: IPR003116; .
DR Pfam: PF00613; RGS; 1.
DR Pfam: PF02196; RBD; 1.
DR SMART: SM00390; GOLOCO; 1.
FT VARIANT 18 18 R -> S.
FT VARIANT 19 19 N -> K.
FT VARIANT 56 56 G -> E.
SQ SEQUENCE 1175 AA; 129802 MW; 8E344F7321DB30F5 CRC64;

Query Match 3.9%; Score 172.5; DB 5; Length 1175;
Best Local Similarity 19.1%; Pred. No. 0.00057;
Matches 166; Conservative 136; Mismatches 349; Indels 217; Gaps 36;
OY 40 VGKYSTKPMYSSNARNEDGLGEPGRASPDSP/LTRWTSLSHSLGDQDGAVALFFRTFL 99
DB 426 VPKVLTTPAPSAITVASVAEGAQDHG--CPSS-----WAGSFEMLDADAQMCFSEFL 479

OY 100 EREKCVDTLDFWPAFCNGFRQNLKDTKTLRVAKA--IYKRIENSV-----VSKOLKPAT 153
DB 480 KKEPSAENITFWTACERR--LLESEADRYAQAELIETPAKHLANNSSDPVAVDSOARSLT 536
OY 154 KTYIRDGIRKQOIGSVMDAQTEIOAVEMENAVOVFLTSDIYLEVYSGGENTAYNSNG 213
DB 537 EEKLDADAPD-----IFAPAKOIFSLMKPDSVORFTRSDLYKSCVABEKNODPLPSG 590
OY 214 -GLSLKYLGLPTLNEEEMTCADLKCSLPTVVGSLSTLRATASVSTETAEKNGFR 272
DB 591 LDLELLKTNFHLGAFSKLKK-SASNAEDRRKSLPMPHRRKT--RSKSRDTEIADMQH 647
OY 273 SFKSDPVNRYHVGSGYFAPATSAN-----DSLTSDALTDOSMTDSSVQDPVPR 326
DB 648 ALMPAPV-PQN-----APLTSASLKVCGONSLSLHSSRSSFSFA---GTATGG 696
OY 327 MGSKQLOREHMRSVKANGOVSLPHFPRTHRLPKEMTEVEPAFAFADLSRLKLELE 386
DB 697 OGASTESVYSLCRVILTDGATTI-----VOTRGETVGLVERL-----LE 737
OY 387 SRHSLERLQOIREDDEKESBQALSSRDGAPVONPLALLPSGTYEEDPOTILLDHLSTV 446
DB 738 KRN-----LVPRYDIVFGSTKSID-----VQPSQILAG-----KEVIERRVAFK 780
OY 447 LKTPGCSPGVGRVSPRSRDPDHHQ-----HHHHOCHTL----- 483
DB 781 LDRP--DPKV--ISVSKPKQLHEVIRPLISKYNYMEQVOVIMRPTOVPIDLNQVPT 835
OY 484 -----STGKLRPVACRLGKSEFLTKOTTKHVHHYIHHNAVPT 525
DB 836 MADGRLRIYVNSDFVGGSSMPKQSKPKRLPGCHLDELTKVFNELLASKA----- 891
OY 526 KEELIATATORVRLCLPGCTDYCYCSKSHPKAPRLPGEOFGSROGTLPRKNAKTE 585
DB 892 -----DAAASE-----KSRP-----VLCMSKSNAPSESSLFE 921
OY 586 PGLALSARDGSMSSAAGPOL-----PGEGRSDQDVMQ-----WMLE 623
DB 922 -RMROORDGDNIPASKLPKLKKSTSSQOSEEAATGTAVDPKPKLIAKLKAGVKLOV 980
OY 624 SEROSKSPHSAOSIRKSY--PLESARA-----PGEVRNHLGLGASHRSV-ARAH 674
DB 981 TERVAEHOEDELLEGLKRAQLARLEDQRTETINFDLPRLKKNENISAUVSKLRKVASLS 1040
OY 675 PFTODPAMPRLTPNTLAOLEBACRLAEVSKPQORCCVASQQRDRHNSAAGASPF 734
DB 1041 PVSIVPATP-----TEIQPAPRLSITRSQOPVSPMKVDOEBETDLPAATQ-DQTEF 1091
OY 735 AN--PSLAPEDHKEPKLASVHALQASLVVTFPCGEEIYRRM-----LKAQ 781
DB 1092 AKAPRPLPPKPKVLPKPSNMGVAOP-----TGNYCNKYSPOKVPSPKESKPTGTFAS 1146
OY 782 SLTLGHFEOLSKKGNRYEYFKKASDEF 809
DB 1147 KIPLDLGRKSLLEAGSCAVILDEPSSSF 1174

RESULT 13
O9JL24 PRELIMINARY; PRT; 211 AA.
AC O9JL24;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OY NCBI_TaxID=10090;
R [1]
I SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=EMBRYO;

